

☒ Drafts

☒ Pending

☒ Active

☒ Failed

☒ Saved

☒ S1: (162) KATO-SEISHI.in. SEKINE-SHINGO.in. SEKINE-SHINGO-NISHIOONUNA.in. YAMAGUCHI-TOMOKI.in. YA...

☒ S2: (18932) 530/350.ccls.

☒ S3: (10) S1 and S2

☒ S5: (162) KATO-SEISHI.in. SEKINE-SHINGO.in. SEKINE-SHINGO-NISHIOONUNA.in. YAMAGUCHI-TOMOKI.in. YA...

☒ S6: (5) S4 and S5

☒ S4: (3902) TM4

☒ S8: (18465) 530/350.ccls.

☒ S9: (9) S5 and S8

☒ S11: (1) "6054289".pr

☒ Favorites

☒ Tagged (1)

☒ UDC

☒ Queue

☒ Trash

EAST Search 4/5/06
P116

BEST AVAILABLE COPY

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 4, 2006, 21:31:55 ; Search time 7.5 Seconds
(without alignments)
1673.356 Million cell updates/sec

Title: US-10-608-388A-1

Perfect score: 1429

Sequence: 1 atgggccagcgccatcac.....tccactggcggaacctatgca 759

Scoring table: BLOSUM62

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| Xgapop 10.0 , Xgapext 0.5 |
| Fgapop 10.0 , Fgapext 0.5 |
| Dgapop 6.0 , Dgapext 7.0 |
| Delop 6.0 , Delext 7.0 |

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/abss/ABSSWEB.spool/US10608388/runat_04042006_150655_14135/app_query.fasta_1
-DB=issued Patents AA -QPMT=fastan -SUFFIX=n2p.ra1 -MINMATCH=0.1 -LOOPCL=0
-LDOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02p -USER=US10608388 @CGN1_1_71 @runat_04042006_150655_14135
-NCPU=6 -ICPU=3 -NO_WMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pcp.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pcp.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pcp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 1300 | 91.0 | 252 | 2 | US-08-705-771-17 |
| 2 | 1300 | 91.0 | 252 | 2 | US-09-417-540-17 |
| 3 | 453 | 31.7 | 222 | 2 | US-10-037-417-81 |
| 4 | 344 | 24.1 | 253 | 2 | US-09-333-599-4 |
| 5 | 344 | 24.1 | 253 | 2 | US-09-499-781-4 |
| 6 | 343.5 | 24.0 | 249 | 2 | US-09-949-016-8334 |
| 7 | 333.5 | 23.3 | 267 | 2 | US-09-949-016-9088 |
| 8 | 333.5 | 23.3 | 275 | 2 | US-09-949-016-8346 |
| 9 | 332 | 23.2 | 253 | 2 | US-09-333-599-2 |
| 10 | 332 | 23.2 | 253 | 2 | US-09-499-781-2 |
| 11 | 332 | 23.2 | 276 | 2 | US-09-949-016-8972 |
| 12 | 329 | 23.0 | 245 | 2 | US-10-012-231A-4 |

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| 13 | 329 | 23.0 | 245 | 2 | US-10-015-389A-4 | Sequence 4, Appli |
| 14 | 329 | 23.0 | 245 | 2 | US-10-006-768A-4 | Sequence 4, Appli |
| 15 | 329 | 23.0 | 245 | 2 | US-10-015-671A-4 | Sequence 4, Appli |
| 16 | 329 | 23.0 | 245 | 2 | US-10-015-393A-4 | Sequence 4, Appli |
| 17 | 329 | 23.0 | 245 | 2 | US-10-011-833A-4 | Sequence 4, Appli |
| 18 | 329 | 23.0 | 245 | 2 | US-10-006-041A-4 | Sequence 4, Appli |
| 19 | 329 | 23.0 | 245 | 2 | US-10-012-064A-4 | Sequence 4, Appli |
| 20 | 303 | 21.2 | 255 | 2 | US-09-949-016-9861 | Sequence 9861, Ap |
| 21 | 301.5 | 21.1 | 238 | 2 | US-09-949-016-6334 | Sequence 6334, Ap |
| 22 | 299.5 | 21.0 | 222 | 2 | US-09-949-016-8347 | Sequence 8347, Ap |
| 23 | 297.5 | 20.8 | 280 | 2 | US-09-949-016-7296 | Sequence 7296, Ap |
| 24 | 297.5 | 20.8 | 270 | 2 | US-09-949-016-9117 | Sequence 9117, Ap |
| 25 | 285 | 19.9 | 265 | 1 | US-08-807-044-1 | Sequence 1, Appli |
| 26 | 283 | 19.8 | 267 | 2 | US-08-430-225A-20 | Sequence 20, Appl |
| 27 | 283 | 19.8 | 267 | 2 | US-09-795-380-20 | Sequence 20, Appl |
| 28 | 273.5 | 19.1 | 219 | 1 | US-08-855-140-3 | Sequence 3, Appli |
| 29 | 273.5 | 19.1 | 219 | 1 | US-08-807-044-3 | Sequence 3, Appli |
| 30 | 273.5 | 19.1 | 219 | 4 | PCT-US91-04986-2 | Sequence 2, Appli |
| 31 | 273.5 | 19.1 | 231 | 2 | US-09-949-016-10626 | Sequence 10626, A |
| 32 | 271 | 19.0 | 280 | 1 | US-08-855-140-1 | Sequence 1, Appli |
| 33 | 270.5 | 18.9 | 219 | 1 | US-08-855-140-4 | Sequence 4, Appli |
| 34 | 263 | 18.4 | 241 | 2 | US-08-808-148-1 | Sequence 1, Appli |
| 35 | 263 | 18.4 | 241 | 2 | US-09-020-956-114 | Sequence 114, App |
| 36 | 263 | 18.4 | 241 | 2 | US-09-030-607-114 | Sequence 114, App |
| 37 | 263 | 18.4 | 241 | 2 | US-09-439-313-114 | Sequence 114, App |
| 38 | 263 | 18.4 | 241 | 2 | US-09-352-616A-114 | Sequence 114, App |
| 39 | 263 | 18.4 | 241 | 2 | US-09-232-149A-114 | Sequence 114, App |
| 40 | 263 | 18.4 | 241 | 2 | US-09-159-812-114 | Sequence 114, App |
| 41 | 263 | 18.4 | 241 | 2 | US-09-636-215-114 | Sequence 114, App |
| 42 | 263 | 18.4 | 241 | 2 | US-09-685-166A-114 | Sequence 114, App |
| 43 | 263 | 18.4 | 241 | 2 | US-09-115-453-114 | Sequence 114, App |
| 44 | 263 | 18.4 | 241 | 2 | US-09-688-489-114 | Sequence 114, App |
| 45 | 263 | 18.4 | 241 | 2 | US-09-679-426-114 | Sequence 114, App |

ALIGNMENTS

RESULT 1
US-08-705-771-17

Sequence 17, Application US/08705771
Patent No. 6054289
GENERAL INFORMATION:
APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
APPLICANT: Jian Ni and Jing-Shan Hu
TITLE OF INVENTION: Human Genes, Sequences and
TITLE OF INVENTION: Expression Products
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,771
FILING DATE: August 30, 1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-346 (PFI96)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
TELEFAX: 973-994-1744
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:

LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-705-771-17

Alignment Scores:
Pred. No.: 4,65e-138 Length: 252
Score: 1300.00 Matches: 252
Percent Similarity: 98.8% Conservativity: 0
Best Local Similarity: 98.8% Mismatches: 0
Query Match: 91.0% Indels: 3
DB: 2 Gaps: 0

US-10-608-388A-1 (1-759) x US-08-705-771-17 (1-252)

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DB 1 MetGlyGlnCysGlyIleThrSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
QY 61 TGGGGGGGAGCTGGGCAATTTATGCTATGTGGAGCGCTATGCTTCATCACTATGATGAC 120
DB 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACCACTCTTTGAAGATGTGTACACGCTCATCTCTGTAGTGTATGATCATCTGTA 180
DB 41 TyrAspHisPhePheGluaspValTyrThrLeuIleProAlaValIleIleAlaVal 60
QY 181 GGAGCGCTCTTTTCATCATTTGGCTAATGGCTGTGCTGCCACAAATCGGGAAGTGGC 240
DB 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysAlaThrIleArgGluSerArg 80
QY 241 TGTGACTTGGCACTGTTGTATCATCTCTCTGCTCTGCTTTGTGCAGAGTTGTTGTA 300
DB 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
QY 301 GTGGTTTGGGATATCTTTACAGACCAAGTGGAAATGAGTTGATCGCAGCACTTCAG 360
DB 101 ValValLeuGlyTyrValTyrArgAlaIysValGluAsnGluValAspArgSerIleGln 120
QY 361 AAAGTGATATAAGACCTTACAAATGGAAACCAACCTGTATGCTGTAGCGGGCTATTGATT 420
DB 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGACACACTGATGTTGTGAATTCACACTCTCAGACTCGGGAATACAGAT 480
DB 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
QY 481 TGGTTCAAGAACCAAAACCAAGACGAGTGCCCTCTAGCTGTGCGAGAGACTGCCAGC 540
DB 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysArgGluThrAlaSer 180
QY 541 AATTGTAATGGCAGCTGGCCCAACCTCTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
DB 181 AsnCysAsnGlySer-Trip-ProProPheArg-LeuTyrAlaGluGlyCysGluAlaLeu 199
QY 601 GTAGTGAAGAGCTACAAGAAATCATGATGTCATGTGATCTGGCGCCCACTGGCAATTGCA 660
DB 200 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 219
QY 661 GCTATTACCTCTGGGCACTGCTGTGCTCTGCATCGTCTGTGCAGAGAGGATGAGAT 720
DB 220 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 739
QY 721 CCTGCTTACGAGCTCTCATCTACTGGCGGAACCTATGCA 759
DB 240 ProIleTyrGluLeuLeuIleThrGlyGlyThrTyrAla 252
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RESULT 2

US-09-417-540-17

Sequence 17, Application US/09417540

Patent No. 6639052

GENERAL INFORMATION:

APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
Jian Ni and Jing-Shan Hu
TITLE OF INVENTION: Human Genes, Sequences and
Expression Products
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,540
FILING DATE: 14-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,771
FILING DATE: August 30, 1996
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
TELEFAX: 973-994-1744
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-417-540-17

Alignment Scores:
Pred. No.: 4,65e-138 Length: 252
Score: 1300.00 Matches: 252
Percent Similarity: 98.8% Conservativity: 0
Best Local Similarity: 98.8% Mismatches: 0
Query Match: 91.0% Indels: 3
DB: 2 Gaps: 0

US-10-608-388A-1 (1-759) x US-09-417-540-17 (1-252)

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QY 1 ATGGGCGGAGTGGGCGATCACCTCTCCAGACCGTGGTCTTTCTCAACCTCATCTTC 60
DB 1 MetGlyGlnCysGlyIleThrSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
QY 61 TGGGGGGGAGCTGGGCAATTTATGCTATGTGGAGCGCTATGCTTCATCACTATGATGAC 120
DB 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACCACTCTTTGAAGATGTGTACACGCTCATCTCTGTAGTGTATGATCATCTGTA 180
DB 41 TyrAspHisPhePheGluaspValTyrThrLeuIleProAlaValIleIleAlaVal 60
QY 181 GGAGCGCTCTTTTCATCATTTGGCTAATGGCTGTGCTGCCACAAATCGGGAAGTGGC 240
DB 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysAlaThrIleArgGluSerArg 80
QY 241 TGTGACTTGGCACTGTTGTATCATCTCTCTGCTCTGCTTTGTGCAGAGTTGTTGTA 300
DB 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
QY 301 GTGGTTTGGGATATCTTTACAGACCAAGTGGAAATGAGTTGATCGCAGCACTTCAG 360
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QY 427 AGACAGCTGATGTTGGATTTCAACACTACTCAGACTGGGAAATACAGATTGGTTC 486
Db 151 GlnGluPheHisCysGlySerAsnAsnSerGlnAspTrpGlnAspSerGluTrpIle 170
QY 487 AAA-----GAACCAAAACACAGAGTGTCTTACGTGTGTCAGAGAGATGCCAGC 540
Db 171 ArgSerGlyGluAlaAspSerArgValValProAspSerCysGlySerMetValAla 190
QY 541 AATTGAATGGCAGCTGGCCACCTTCGACCTCTAT-----GCTGAGGGGTGGAG 594
Db 191 GlyCys---GlyysArgAspHisAlaSerAsnIleTrpLysValGluGlyGlyCysIle 209
QY 595 GCTCTAGTACTGAGAGCTACAGAAATCATGTCATGTCATGTCGGCCGACCTGGCA 654
Db 210 ThrLysLeuGluThrPheIleGlnGluHisLeuArgValIleGlyAlaValGlyIleGly 229
QY 655 TTTCAGCTATTACGTCTGGGCGATGCTGTGTCTTGC 693
Db 230 IleAlaCysValGlnValPheGlyMetIlePheThrCys 242

RESULT 6
US-09-949-016-8334
; Sequence 8334, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8334
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8334

Alignment Scores:
Pred. No.: 5,36e-30 Length: 249
Score: 343.50 Matches: 85
Percent Similarity: 50.2% Conservative: 41
Best Local Similarity: 33.9% Mismatches: 102
Query Match: 24.0% Indels: 23
DB: 2 Gaps: 7

US-10-608-388A-1 (1-759) x US-09-949-016-8334 (1-249)

QY 16 ATCACTCTCCAGACCGTGTGGTCTTCTCAACCTCATCTTCTGGGGGAGCTGGC 75
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QY 76 ATTTATGCTATGTGGAGCGCTATGCTTCATCATCATATGATGACATGACCATCTCTTT 135
Db 32 IleLeuLeuAlaValGlyValTrpGlyLysLeuThrLeuGlyThrTyrIleSerLeuIle 51
QY 136 GAAGATGTACACGCTCAACCTGCTGTAGTATCATGCTGTAGAGCCCTGCTTTTC 195
Db 52 AlaGluAsnSerThrAsnAlaPro---TyrValLeuIleGlyThrGlyThrIleVal 70
QY 196 ATCATTGGCTAATTGGCTGCTGTGCCACATCCGGAAAGTCGTGTGGATTGCCAGC 255
Db 71 ValPheGlyLeuPheGlyCysPheAlaThrCysArgGlySerProTrpMetLeuLysLeu 90
QY 256 TTGTGCATCATCTGCTCTTGTGTTTGTGCACAGAGTGTGTAGTGTGTTGGGATAT 315

Db 91 TyrAlaMetPheLeuSerLeuValPheLeuAlaGluLeuValAlaGlyIleSerGlyPhe 110
QY 316 GTTTACAGAGCAAAAGTGGAAAATAGGTTGATCGCAGCATTCAGAAAGTGTATAAGACC 375
Db 111 ValPheArgHisGluIleLysAspThrPheLeuArgThrTyrThrAspAlaMetGlnThr 130
QY 376 TACAATGGAAACCAACCTCATGCTAGCGGGCTATTGATTATGTACAGACACAGCTG 435
Db 131 TyrAsnGlyAsn-----AspGluArgSerArgAlaValAspHisValGlnArgSerLeu 148
QY 436 CATTTGTGGAAATTCACAACTACTCAGACTGGGAAATACAGATTGGTTCAAAGAAACC 495
Db 149 SerCysGlyValGlnAsnTyrThrAsnTrpSerThrSerProTyrPheLeuGlu--- 167
QY 496 AAAACACAGAGTGTCCCTCTTAGCTGCTGACAGAGACTGCCAGCAATGTATGGCAGC 555
Db 168 -----HisGlyIleProProSerCysCysMet---AsnGluThrAspCysAsn----- 182
QY 556 CTGGCCCACTTCGACCTCTAT-----GCTGAG 585
Db 183 -----ProGlnAspLeuHisLeuThrValAlaAlaThrLysValAsnGlnLys 199
QY 586 GGGTGTGAGGCTCTAGTAGTGAAGAGCTACAGAAATCATGATCATGTGATCTGGGCC 645
Db 200 GlyCysTyrAspLeuValThrSerPheMetGluThrAsnMetGlyIleIleAlaGlyVal 219
QY 646 GCACTGGCATTTGCCAGCTATTACAGCTGTGGGCACTGCTGTGCTGTCATCGTTGTGC 705
Db 220 AlaPheGlyIleAlaPheSerGlnLeuIleGlyMetLeuLeuAlaCys---CysLeuSer 238
QY 706 AGAAGAGTAGAGATCCTGCTTACGAGCTCCTC 738
Db 239 ArgPheIleThrAlaAsnGlnTyrGluMetVal 249

RESULT 7

US-09-949-016-9088
; Sequence 9088, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9088
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9088

Alignment Scores:

Pred. No.: 7,43e-29 Length: 267
Score: 333.50 Matches: 78
Percent Similarity: 50.0% Conservative: 46
Best Local Similarity: 31.5% Mismatches: 101
Query Match: 23.3% Indels: 23
DB: 2 Gaps: 6

US-10-608-388A-1 (1-759) x US-09-949-016-9088 (1-267)

QY 16 ATCACTCTCCAGACCGTGTGGTCTTCTCAACCTCATCTTCTGGGGGAGCTGGC 75

Db 36 IleThrCysPheLysSerValLeuLeuIleTyrThrPheIlePheTrpIleThrGlyVal 55

76 ATTTTATGCTAGTGGGAGCCTATGCTTCATCATCACTTATGATGACTATGACACACTTCCTTT 135
 56 IleLeuLeuAlaValGlyIlePrpGlyLysValSerLeuGluAsnTyrPheSerLeuLeu 75
 136 GAAGATGTGTACACGCTCATCCCTGCTGTAGTGATCATAGCTGTAGGAGCCCTGCTTTTC 195
 76 AsnGluLysAlaThrAsnValPro--PheValLeuIleAlaThrGlyThrValIleIle 94
 196 ATCATTTGGCGTAATTGGCTGTGTCGCCAAATCCGGGAAAGCGCTGTGGAGCTGCCACG 255
 95 LeuLeuGlyThrPheGlyCysPheAlaThrCysArgAlaSerAlaTrpMetLeuLysLeu 114
 256 TTTGTTCATCATCCTCTCTGTGTTTTTGTGCACAGAGTTGTTGTAGTGTGTTTGGATAT 315
 115 TyrAlaMetPheLeuThrLeuValPheLeuValGluLeuValAlaAlaIleValGlyPhe 134
 316 GTTTACAGACGAAAGGTGGAAATGAGGTTGATCGCAGCATTCAGAAAGTGTATTAAGACC 375
 135 ValPheArgHisGluIleLysAsnSerPheLysAsnAsnTyrGluLysAlaLeuLysGln 154
 376 TACAAATGGAACCAACCTGTAGCTGCTAGCGGGCTATTGATTATGATACAGACAGACAGTG 435
 155 TyrAsnSerThrGly--AspTyrArgSerHisAlaValAspLysIleGlnAsnThrLeu 173
 436 CATTTGTTGTGAATTCACAACTACTCAGACTCGGAAATACAGATTGTTTCAAGAAACC 495
 174 HisCysCysGlyValThrAspTyrArgAspTrpThrAspThrAsnTyrTyrSerGlu--- 192
 496 AAAAACCAGAGTGTCCCTCTTAGCTGTCTGCAGA-----GAGACT 534
 193 -----LysGlyPheProLysSerCysCysLysLeuGluAspCysThrProGlnArgAsp 210
 535 GCCAGCAATTGTAATGGCAGCCTGGCCACCCTTCGACCTCATGCTGAGGGGTGTGAG 594
 211 AlaAspLysValAsnAsn-----GluclyCysPhe 220
 595 GCTCTAGTAGTGAAGAAGCTACAGAATCATATGATGTCATGTGATCTGGGCCCGCATGGCA 654
 221 IleLysValMetThrIleIleIleGluSerGluMetGlyValValAlaGlyIleSerPheGly 240
 655 TTTGCAGCTATTTCAGCTCTGGGCACTGCTGTGCTTGCATCGTGTGTCAGAGGAGGT 714
 241 ValAlaCysPheGlnLeuIleIleGlyIlePheLeuAla---TyrCysLeuSerArgAlaIle 259
 715 AGATATCCTGTATTACAGACTCCTC 738
 260 ThrAsnAsnGlnTyrGluIleVal 267

RESULT 8
US-09-949-016-8346
; Sequence 8346, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8346
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8346

| Alignment Scores: | 7.52e-29 | Length: | 275 |
|---|----------|---|-----|
| Pred. No.: | 333.50 | Matches: | 78 |
| Score: | 50.0% | Conservative: | 46 |
| Percent Similarity: | 31.5% | Mismatches: | 101 |
| Best Local Similarity: | 23.3% | Indels: | 23 |
| Query Match: | 2 | Gaps: | 6 |
| DB: | | | |
| US-10-608-388A-1 (1-759) x US-09-949-016-8346 (1-275) | | | |
| Qy | 16 | ATCACCTCTCAAGACGGTCTGGTCTTTCTCAACCTCATCTTCTGGGGCAGCTGC | 75 |
| Db | 44 | IleThrCysPheLysSerValLeuLeuIleTyrThrPheIlePheTyrIleThrGlyVal | 63 |
| Qy | 76 | ATTTTATGCTATGTTGGAGCCATGCTTTCATCATCTATGATCATGACCATGACCTCTTT | 135 |
| Db | 64 | IleLeuLeuAlaValGlyIleTyrGlyLysValSerLeuGluAsnTyrPheSerLeuLeu | 83 |
| Qy | 136 | GAAGATGTACACGGCTCATCCCTGCTGTAGTGATCATAGCTGTAGGACCCCTGCTTTTC | 195 |
| Db | 84 | AsnGluLysAlaThrAsnValPro--PheValLeuIleAlaThrGlyThrValIleIle | 102 |
| Qy | 196 | ATCATGGGCTAATGGCTGTGTGCCAATCCGGGAAAGTCGGCTGTGGACTTGGCCAGC | 255 |
| Db | 103 | LeuLeuGlyThrPheGlyCysPheAlaThrCysArgAlaSerAlaTyrMetLeuLysLeu | 122 |
| Qy | 256 | TTTGTCTATCATCTGCTCTCGTTTTTCTTCACAGAAAGTTGTGTAGTGGTTTGGGATAT | 315 |
| Db | 123 | TyrAlaMetPheLeuThrLeuValPheLeuValGluLeuValAlaAlaIleValGlyPhe | 142 |
| Qy | 316 | GTTTACAGACGAAAGTGGAAAATGAGGTTGATCCGAGCATTCAGAAAGTGTATAAGACC | 375 |
| Db | 143 | ValPheArgHisGluIleLysAsnSerPheLysAsnAsnTyrGluLysAlaLeuLysGln | 162 |
| Qy | 376 | TAGAAATGGAACCAACCCCTGATCTGCTAGACGGGCTATTGATTATCTACAGACACAGCTG | 435 |
| Db | 163 | TyrAsnSerThrGly--AspTyrArgSerHisAlaValAspLysIleGlnAsnThrLeu | 181 |
| Qy | 436 | CATTGTTGTGGAATTCACAACTACTCAGACTGGGAAAATACAGATTGGTTCAAAGAAACC | 495 |
| Db | 182 | HisCysCysGlyValThrAspTyrArgAspTyrThrAspThrAsnTyrTyrSerGlu-- | 200 |
| Qy | 496 | AAAAACAGAGTGTCCTCTTAGCTGCTGCAGA-----GAGACT | 534 |
| Db | 201 | -----LysGlyPheProLysSerCysCysLysLeuGluAspCysThrProGlnArgAsp | 218 |
| Qy | 535 | GCCAGCAATTCATATGGCAGCTGGCCCAACCCCTCCGACCTCTATGCTGAGGGGTGTGAG | 594 |
| Db | 219 | AlaAspLysValAsnAsn-----GluGlyCysPhe | 228 |
| Qy | 595 | GCTCTATGATGTGAAGAGCTCAAGAAATCATGATGCTATGATCTGGGCCGACCTGGCA | 654 |
| Db | 229 | IleLysValMetThrIleIleGluSerGluMetGlyValValAlaGlyIleSerPheGly | 248 |
| Qy | 655 | TTTTCAGCTATTTCAGCTCTGGGCAATGCTGTGCTTGCATCGTGTGTGCAGAGGAGT | 714 |
| Db | 249 | ValAlaCysPheGlnLeuIleGlyIlePheLeuAla---TyrCysLeuSerArgAlaIle | 267 |
| Qy | 715 | AGAGATCTGCTTACGAGCTCCTC | 738 |
| Db | 268 | ThrAsnAsnGlnTyrGluIleVal | 275 |

RESULT 9
US-09-333-599-2
; Sequence 2, Application US/09333599
; Patent No. 6245898
; GENERAL INFORMATION:
; APPLICANT: Testa, Jacqueline E.
; APPLICANT: Quigley, James P.
; APPLICANT: Seandel, Marco
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES THAT RECOGNIZE ANTIGENS
; TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS
; FILE REFERENCE: SUNY

; CURRENT APPLICATION NUMBER: US/09/333,599
; CURRENT FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-333-599-2

Alignment Scores:
Pred. No.: 1.07e-28 Length: 253
Score: 332.00 Matches: 67
Percent Similarity: 51.1% Conservative: 52
Best Local Similarity: 28.8% Mismatches: 108
Query Match: 23.2% Indels: 6
DB: 2 Gaps: 4

US-10-608-388A-1 (1-759) x US-09-333-599-2 (1-253)

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QY 10 TGGGGCATCCTCTCCAGACCGTGTGCTCTTCTCAACCTCATCTTCTGGGGGCA 69
    ||||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 11 CysGlyThrValCysLeuLysTyLeuLeuPheThrTyraSncCysCysPheTrpLeuAla 30
    ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 70 GCTGGCATTATGCTATGCGGAGCCCTATGCTTTCATCACTTATGATGACTATGACCAC 129
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 31 GlyLeuAlaValMetAlaValGlyIleTrpThrLeuAlaLeuLysSerAspTyriLeSer 50
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 130 TTCTTTGAAGATGTATACAGCTCATCCCTGCTGTAGTATCATPAGTGTAGGAGCCCTG 189
    ||||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 51 LeuLeuAlaSerGlyThrTyLeuAlaThrAlaTyriLeuValAlaGlyThrVal 70
    ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 190 CTTTTCATCATGCGCTAATGCTGCTGTGCCAATCCGGAAGTCCGCTGGACTT 249
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 71 ValMetValThrGlyValLeuGlyCysCysAlaThrPheLysGluArgArgAsnLeuLeu 90
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 250 GCCACGTTTTCATCTCTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 309
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 91 ArgLeuTyriPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 110
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 310 GGATATGTTTACAGACAAAGTGGAAATGAGTTGATCGCAGCATTCAG---AAAGTG 366
    ||||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 111 AlaTyriAlaTyriTyriGlnGlnLeuAsnThrGluLeuLysGluAsnLeuLysAspThrMet 130
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 367 TATAAGACCTACATGAACCAACCTGCTGTAGTGTAGTGTAGTGTATGATGATGATGATG 426
    ||||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 131 ThrLysArgTyriHisGlnProGlyHisGluAlaValThrSerAlaValAspGlnLeuGln 150
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 427 AGACAGCTGATTTGTGGAATTCACAACTACTCAGCTGGGAAATACAGATTGTTTC 486
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 151 GlnGluPheHisCysCysGlySerAsnAsnSerGlnAspTrpArgAspSerGluTrpIle 170
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 487 AAA-----GAAACCAAAACACAGAGTGTCCCTTTAGCTGTGCAGAGAGATGCCAGC 540
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 210 ThrLysLeuGluThrPheIleGlnGluHisLeuArgValIleGlyAlaValGlyIleGly 229
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 655 TTTCAGCTATTACGCTGGCGCATGCTGTGTGTGCTTGC 693
    ||||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 230 IleAlaCysValGlnValPheGlyMetIlePheThrCys 242
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
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RESULT 10

US-09-499-781-2
; Sequence 2, Application US/09499781
; Patent No. 6498014
; GENERAL INFORMATION:

; APPLICANT: Testa, Jacqueline E.
; APPLICANT: Quigley, James P.
; APPLICANT: Seandel, Marco
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES THAT RECOGNIZE ANTIGENS
; TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS
; FILE REFERENCE: SUNY
; CURRENT APPLICATION NUMBER: US/09/499,781
; CURRENT FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 09/333,599
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-781-2

Alignment Scores:
Pred. No.: 1.07e-28 Length: 253
Score: 332.00 Matches: 67
Percent Similarity: 51.1% Conservative: 52
Best Local Similarity: 28.8% Mismatches: 108
Query Match: 23.2% Indels: 6
DB: 2 Gaps: 4

US-10-608-388A-1 (1-759) x US-09-499-781-2 (1-253)

```
QY 10 TGGGGCATCCTCTCCAGACCGTGTGCTCTTCTCAACCTCATCTTCTGGGGGCA 69
    ||||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 11 CysGlyThrValCysLeuLysTyLeuLeuPheThrTyraSncCysCysPheTrpLeuAla 30
    ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 70 GCTGGCATTATGCTATGCGGAGCCCTATGCTTTCATCACTTATGATGACTATGACCAC 129
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 31 GlyLeuAlaValMetAlaValGlyIleTrpThrLeuAlaLeuLysSerAspTyriLeSer 50
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 130 TTCTTTGAAGATGTATACAGCTCATCCCTGCTGTAGTATCATPAGTGTAGGAGCCCTG 189
    ||||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 51 LeuLeuAlaSerGlyThrTyriLeuAlaThrAlaTyriLeuValAlaGlyThrVal 70
    ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 190 CTTTTCATCATGCGCTAATGCTGCTGTGCCAATCCGGAAGTCCGCTGGACTT 249
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 71 ValMetValThrGlyValLeuGlyCysCysAlaThrPheLysGluArgArgAsnLeuLeu 90
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 250 GCCACGTTTTCATCTCTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 309
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 91 ArgLeuTyriPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 110
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 310 GGATATGTTTACAGACAAAGTGGAAATGAGTTGATCGCAGCATTCAG---AAAGTG 366
    ||||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 111 AlaTyriAlaTyriTyriGlnGlnLeuAsnThrGluLeuLysGluAsnLeuLysAspThrMet 130
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 367 TATAAGACCTACATGAACCAACCTGCTGTAGTGTAGTGTAGTGTATGATGATGATGATG 426
    ||||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 131 ThrLysArgTyriHisGlnProGlyHisGluAlaValThrSerAlaValAspGlnLeuGln 150
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 427 AGACAGCTGATTTGTGGAATTCACAACTACTCAGCTGGGAAATACAGATTGTTTC 486
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 151 GlnGluPheHisCysCysGlySerAsnAsnSerGlnAspTrpArgAspSerGluTrpIle 170
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 487 AAA-----GAAACCAAAACACAGAGTGTCCCTTTAGCTGTGCAGAGAGATGCCAGC 540
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 171 ArgSerGlnGluAlaGlyGlyArgValValProAspSerCysCysLysThrValAla 190
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 541 AATTGTAATGGCAGCTGGCGCCACCTTCCGACCTCTAT-----GCTGAGGGGTGTGAG 594
    ||||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 191 LeuCys---GlyGlnArgAspHisAlaSerAsnIleTyriLysValGluGlyCysIle 209
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 595 GCTCTAGTAGTAGAGAGCTACAGAAATCATGATGATGATGATGATGATGATGATGATG 654
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 210 ThrLysLeuGluThrPheIleGlnGluHisLeuArgValIleGlyAlaValGlyIleGly 229
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 655 TTTCAGCTATTACGCTGGCGCATGCTGTGTGTGCTTGC 693
    ||||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```



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Alignment Scores:
Pred. No.: 2,32e-28 Length: 245
Score: 329.00 Matches: 74
Percent Similarity: 50.4% Conservative: 43
Best Local Similarity: 31.9% Mismatches: 93
Query Match: 23.0% Indels: 22
DB: 2 Gaps: 5

US-10-608-388A-1 (1-759) x US-10-012-231A-4 (1-245)
QY 16 ATCACTCTCCCAAGACCGTGGTCTTTCTCAACCTCATCTCTGGGGGGGAGCTGGC 75
Db 14 ILeThrCysPheLysSerValLeuLeuIleThrPheIlePheThrGlyVal 33
QY 76 ATTTATGCTATGGGAGCGCTATGCTTTCATCACTTATGATGACTATGACCTTTT 135
Db 34 ILeLeuLeuAlaValGlyIleTrpGlyLysValSerLeuGluAsnTyrPheSerLeuLeu 53
QY 136 GAAGATGTGTACAGCTCATCCCTGCTGTAGTATCATAGCTGTAGGAGCCCTGCTTTTC 195
Db 54 AsnGluLysAlaThrAsnValPro---PheValLeuIleAlaThrGlyThrValIleIle 72
QY 196 ATCATGGGCTAATGGCTGCTGTGCACAAATCCGGGAAAGTCGCTGTGAGCTTGCACG 255
Db 73 LeuLeuGlyThrPheGlyCysPheAlaThrCysArgAlaSerAlaTrpMetLeuLysLeu 92
QY 256 TTGTGTCATCTCTGCTCTTGGTTTGTACAGAGTCTTGTAGTGGTGTGGGATAT 315
Db 93 TyrAlaMetPheLeuThrLeuValPheLeuValGluLeuValAlaIleValGlyPhe 112
QY 316 GTTTACAGACAAAGTGGAAATGAGTTGATCGCAGCATTCAGAAAGTGATAGAC 375
Db 113 ValPheArgHisGluIleLysAsnSerPheLysAsnAsnTyrGluLysAlaLeuLysGln 132
QY 376 TACAATGAACCAACCTGATGCTGTGAGCGGCTATTGATATGATGACAGACAGCTG 435
Db 133 TyrAsnSerThrGly---AspTyrArgSerHisAlaValAspLysIleGlnAsnThrLeu 151
QY 436 CATTTGTGGAATTCACACTACTCAGCTGGAAGAAATACAGATTGTTCAAGAAACC 495
Db 152 HisCysGlyValThrAspTyrArgAspTrpThrAspThrAsnTyrTyrSerGlu--- 170
QY 496 AAAAAACAGAGTGCTCTTCTAGCTGCTGCAGA-----GAGACT 534
Db 171 -----LysGlyPheProLysSerCysCysLysLeuGluAspCysThrProGlnArgAsp 188
QY 535 GCCAGCAATTTAATGTCAGCGCTGGCCACCCCTTCCGACCTCTATGCTGAGGGGTGTGAG 594
Db 189 AlaAspLysValAsnAsn-----GluGlyCysPhe 198
QY 595 GCTCTAGTGTGAAGAGCTACAAGAAATCATGATGATGATGCTGGGCGGACCTGGCA 654
Db 199 IleLysValMetThrIleIleGluSerGluMetGlyValValAlaGlyIleSerPheGly 218
QY 655 TTTCGACCTATTGAGCTGCTGGGATCGTGTGCT 690
Db 219 ValAlaCysPheGlnLeuIleGlyIlePheLeuAla 230

RESULT 13
US-10-015-389A-4
; Sequence 4, Application US/10015389A
; Patent No. 6938436
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
```

```
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC48
; CURRENT APPLICATION NUMBER: US/10/015,389A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 4
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-42
; OTHER INFORMATION: Signal Peptide
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: 19-42, 61-83, 92-114, 209-230
; OTHER INFORMATION: Transmembrane Domains
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 69-80, 211-222
; OTHER INFORMATION: Prokaryotic Membrane Lipoprotein Lipid Attachment Site.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 75-81, 78-84, 210-216, 214-220, 226-232
; OTHER INFORMATION: N-Myristoylation Site.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 134-138
; OTHER INFORMATION: N-Glycosylation Site.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 160-168, 160-169
; OTHER INFORMATION: Tyrosine Kinase Phosphorylation Site.
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 233
; OTHER INFORMATION: unknown amino acid
; US-10-015-389A-4
```

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Alignment Scores:
Pred. No.: 2,32e-28 Length: 245
Score: 329.00 Matches: 74
Percent Similarity: 50.4% Conservative: 43
Best Local Similarity: 31.9% Mismatches: 93
Query Match: 23.0% Indels: 22
DB: 2 Gaps: 5
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US-10-608-388A-1 (1-759) x US-10-015-389A-4 (1-245)

```
QY 16 ATCACTCTCCCAAGACCGTGGTCTTTCTCAACCTCATCTCTGGGGGGGAGCTGGC 75
Db 14 ILeThrCysPheLysSerValLeuLeuIleThrPheIlePheThrGlyVal 33
QY 76 ATTTATGCTATGGGAGCGCTATGCTTTCATCACTTATGATGACTATGACCTTTT 135
Db 34 ILeLeuLeuAlaValGlyIleTrpGlyLysValSerLeuGluAsnTyrPheSerLeuLeu 53
QY 136 GAAGATGTGTACAGCTCATCCCTGCTGTAGTATCATAGCTGTAGGAGCCCTGCTTTTC 195
Db 54 AsnGluLysAlaThrAsnValPro---PheValLeuIleAlaThrGlyThrValIleIle 72
QY 196 ATCATGGGCTAATGGCTGCTGTGCACAAATCCGGGAAAGTCGCTGTGAGCTTGCACG 255
Db 73 LeuLeuGlyThrPheGlyCysPheAlaThrCysArgAlaSerAlaTrpMetLeuLysLeu 92
QY 256 TTGTGTCATCTCTGCTCTTGGTTTGTACAGAGTCTTGTAGTGGTGTGGGATAT 315
```

Db 93 TyrAlaMetPheLeuThrLeuValPheLeuValGluLeuValAlaAlaValGlyPhe 112
Qy 316 GTTTACAGAGCAAGGTGGAATGAGTTGATCCAGCATTCAGAAAGTGTATAGACC 375
Db 113 ValPheArgHisGluIleLysAsnSerPheLysAsnAsnTyrGluLysAlaLeuLysGln 132
Qy 376 TACAATGGAACCAACCCGTAGCTGCTAGCCGGCTATTGATTATGTACAGAGACAGCTG 435
Db 133 TyrAsnSerThrGly---AspTyrArgSerHisAlaValAspLysIleGlnAsnThrLeu 151
Qy 436 CATTTGTGGAAATTCACAACTACACTACAGACTGGGAAATACAGATGTGTTCAAGAAACC 495
Db 152 HisCysCysGlyValThrAspTyrArgAspTyrThrAspThrAsnTyrTy-SerGlu--- 170
Qy 496 AAAACACAGAGTGTCCCTTAGCTGCTGCAGC-----GAGACT 534
Db 171 -----LysGlyPheProLysSerCysCysLysLeuGluAspCysThrProGlnArgAsp 188
Qy 535 GCCAGCAATTGTAATGGCAGCGCTGCGCCACCTTCCGACCTCTATGCTGAGGGGTGTGAG 594
Db 189 AlaAspLysValAsnAsn-----GluGlyCysPhe 198
Qy 595 GCTCTAGTAGTGAAGAAGTACAGAAATCATGATGATGATGATGATGATGATGATGATG 654
Db 199 IleLysValMetThrIleIleGluSerGluMetGlyValValAlaGlyIleSerPheGly 218
Qy 655 TTTGACGATTACAGTGTGGGCGATGCTGTGTGCT 690
Db 219 ValAlaCysPheGlnLeuIleGlyIlePheLeuAla 230

RESULT 14

US-10-006-768A-4

; Sequence 4, Application US/10006768A

; Patent No. 6936697

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan I.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830PIC10

; CURRENT APPLICATION NUMBER: US/10/006,768A

; CURRENT FILING DATE: 2002-03-05

; NUMBER OF SEQ ID NOS: 477

; Prior Application removed - See File Wrapper or Palm

; SEQ ID NO 4:

; LENGTH: 245

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: sig_peptide

; LOCATION: 1-42

; OTHER INFORMATION: Signal Peptide

; FEATURE:

; NAME/KEY: TRANSMEM

; LOCATION: 19-42, 61-83, 92-114, 209-230

; OTHER INFORMATION: Transmembrane Domains

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: 69-80, 211-222

; OTHER INFORMATION: Prokaryotic Membrane Lipoprotein Lipid Attachment Site.

; FEATURE:

; NAME/KEY: misc feature
; LOCATION: 75-81, 78-84, 210-216, 214-220, 226-232
; OTHER INFORMATION: N-Myristoylation Site.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 134-138
; OTHER INFORMATION: N-Glycosylation Site.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 160-168, 160-169
; OTHER INFORMATION: Tyrosine Kinase Phosphorylation Site.
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 233
; OTHER INFORMATION: unknown amino acid
US-10-006-768A-4

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 2,32e-28 | Length: | 245 |
| Score: | 329.00 | Matches: | 74 |
| Percent Similarity: | 50.4% | Conservative: | 43 |
| Best Local Similarity: | 31.9% | Mismatches: | 93 |
| Query Match: | 23.0% | Indels: | 22 |
| DB: | 2 | Gaps: | 5 |

US-10-608-388A-1 (1-759) x US-10-006-768A-4 (1-245)

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Qy 76 ATTTTATGCTATGTGGGAGCCTATGCTCTCATCTATGATGATGATGATGATGATGAT 135
Db 34 IleLeuLeuAlaValGlyIleTrpGlyLysValSerLeuGluAsnTyrPheSerLeuLeu 53
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Db 54 AsnGluLysAlaThrAsnValPro---PheValLeuIleAlaThrGlyThrValIleIle 72
Qy 196 ATCACTGGGCTAATGGCTGCTGCCACATCCGGGAAAGTCCGTGTGGGCTGCCACG 255
Db 73 LeuLeuGlyThrPheGlyCysPheAlaThrCysArgAlaSerAlaTrpMetLeuLysLeu 92
Qy 256 TTTGTCATCATCTCTCTTGGTTTTTGTACAGAGTGTGTAGTGTGTGTGTGTGTGTAT 315
Db 93 TyrAlaMetPheLeuThrLeuValPheLeuValGluLeuValAlaAlaIleValGlyPhe 112
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Qy 376 TACAATGGAACCAACCCGTAGCTGCTAGCCGGCTATTGATTATGTACAGAGACAGCTG 435
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Qy 436 CATTTGTGGAAATTCACAACTACTACAGACTGGGAAATACAGATGTGTTCAAGAAACC 495
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Db 171 -----LysGlyPheProLysSerCysCysLysLeuGluAspCysThrProGlnArgAsp 188
Qy 535 GCCAGCAATTGTAATGGCAGCGCTGCGCCACCTTCCGACCTCTATGCTGAGGGGTGTGAG 594
Db 189 AlaAspLysValAsnAsn-----GluGlyCysPhe 198
Qy 595 GCTCTAGTAGTGAAGAAGTACAGAAATCATGATGATGATGATGATGATGATGATGATG 654
Db 199 IleLysValMetThrIleIleGluSerGluMetGlyValValAlaGlyIleSerPheGly 218
Qy 655 TTTGACGATTACAGTGTGGGCGATGCTGTGTGCT 690

Db 219 ValAlaCysPheGlnLeuIleGlyIlePheLeuAla 230
RESULT 15
US-10-015-671A-4
; Sequence 4, Application US/10015671A
; Patent No. 6946263
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C47
; CURRENT APPLICATION NUMBER: US/10/015,671A
; CURRENT FILING DATE: 2001-12-11
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 4
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-42
; OTHER INFORMATION: Signal Peptide
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: 19-42, 61-83, 92-114, 209-230
; OTHER INFORMATION: Transmembrane Domains
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 69-80, 211-222
; OTHER INFORMATION: Prokaryotic Membrane Lipoprotein Lipid Attachment Site.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 75-81, 78-84, 210-216, 214-220, 226-232
; OTHER INFORMATION: N-Myristoylation Site.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 134-138
; OTHER INFORMATION: N-Glycosylation Site.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 160-168, 160-169
; OTHER INFORMATION: Tyrosine Kinase Phosphorylation Site.
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 233
; OTHER INFORMATION: unknown amino acid
US-10-015-671A-4

Alignment Scores:
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Score: 329.00 Matches: 74
Percent Similarity: 50.4% Conservative: 43
Best Local Similarity: 31.9% Mismatches: 93
Query Match: 23.0% Indels: 22
DB: 2 Gaps: 5

US-10-608-388A-1 (1-759) x US-10-015-671A-4 (1-245)

QY 16 ATCACTCTCCAGACGGCTGGTCTTTCTCAACCTCATCTTCTGGGGGCGAGCTGGC 75

Search completed: April 4, 2006, 21:34:23
Job time : 42.5 sec

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 4, 2006, 21:48:29 ; Search time 30.6 Seconds
(without alignments)
2072.761 Million cell updates/sec

Title: US-10-608-388A-1

Perfect score: 1429

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-HEAPSIZES=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10608388 @CGN 1.1 307 @runat_04042006_150706_14321 -NCPU=6 -ICPU=3
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Database : Published Applications AA Main:

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6: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1336 | 93.5 | 253 | 3 | US-09-983-000A-18 |
| 3 | 1336 | 93.5 | 253 | 4 | US-10-223-085-66 |
| 4 | 1336 | 93.5 | 253 | 4 | US-10-223-084-66 |
| 5 | 1336 | 93.5 | 253 | 4 | US-10-223-088-66 |
| 6 | 1336 | 93.5 | 253 | 4 | US-10-223-090-66 |
| 7 | 1336 | 93.5 | 253 | 4 | US-10-223-087-66 |
| 8 | 1336 | 93.5 | 253 | 4 | US-10-223-083-66 |
| 9 | 1336 | 93.5 | 253 | 4 | US-10-223-089-66 |
| 10 | 1336 | 93.5 | 253 | 4 | US-10-223-081-66 |
| 11 | 1336 | 93.5 | 253 | 4 | US-10-223-082-66 |

| | | | | | | |
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| 12 | 1336 | 93.5 | 253 | 4 | US-10-305-654-66 | Sequence 66, Appl |
| 13 | 1336 | 93.5 | 253 | 4 | US-10-081-056-66 | Sequence 66, Appl |
| 14 | 1336 | 93.5 | 253 | 5 | US-10-652-981-18 | Sequence 18, Appl |
| 15 | 1336 | 93.5 | 253 | 5 | US-10-631-467-635 | Sequence 635, Appl |
| 16 | 1332 | 93.2 | 253 | 4 | US-10-156-136-23 | Sequence 23, Appl |
| 17 | 1332 | 93.2 | 253 | 6 | US-11-041-419-23 | Sequence 23, Appl |
| 18 | 1301 | 91.0 | 253 | 5 | US-10-631-467-1431 | Sequence 1431, Appl |
| 19 | 1300 | 91.0 | 252 | 4 | US-10-453-478-17 | Sequence 17, Appl |
| 20 | 453 | 31.7 | 222 | 4 | US-10-037-417-81 | Sequence 81, Appl |
| 21 | 384 | 26.9 | 254 | 3 | US-09-934-268-4 | Sequence 4, Appl |
| 22 | 384 | 26.9 | 254 | 4 | US-10-162-435-38 | Sequence 38, Appl |
| 23 | 384 | 26.9 | 254 | 5 | US-10-860-779-38 | Sequence 38, Appl |
| 24 | 368.5 | 25.8 | 184 | 3 | US-09-930-512-55 | Sequence 55, Appl |
| 25 | 352 | 24.6 | 166 | 3 | US-09-976-782-39 | Sequence 39, Appl |
| 26 | 343.5 | 24.0 | 244 | 4 | US-10-156-136-37 | Sequence 37, Appl |
| 27 | 343.5 | 24.0 | 244 | 5 | US-10-934-998-96 | Sequence 96, Appl |
| 28 | 343.5 | 24.0 | 244 | 6 | US-11-041-419-37 | Sequence 37, Appl |
| 29 | 343.5 | 24.0 | 249 | 5 | US-10-756-149-4994 | Sequence 4994, Appl |
| 30 | 334.5 | 23.4 | 244 | 4 | US-10-205-194-105 | Sequence 105, Appl |
| 31 | 333.5 | 23.3 | 245 | 3 | US-09-823-356-15 | Sequence 15, Appl |
| 32 | 333.5 | 23.3 | 245 | 3 | US-09-729-674-90 | Sequence 90, Appl |
| 33 | 333.5 | 23.3 | 245 | 4 | US-10-156-136-22 | Sequence 22, Appl |
| 34 | 333.5 | 23.3 | 245 | 4 | US-10-024-298A-89 | Sequence 89, Appl |
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| 37 | 333.5 | 23.3 | 245 | 4 | US-10-024-298A-89 | Sequence 89, Appl |
| 38 | 333.5 | 23.3 | 245 | 5 | US-10-913-553-90 | Sequence 90, Appl |
| 39 | 333.5 | 23.3 | 245 | 5 | US-10-696-639-63 | Sequence 63, Appl |
| 40 | 333.5 | 23.3 | 245 | 6 | US-11-041-419-22 | Sequence 22, Appl |
| 41 | 333.5 | 23.3 | 284 | 4 | US-10-106-698-6305 | Sequence 6305, Appl |
| 42 | 332 | 23.2 | 253 | 4 | US-10-153-668-476 | Sequence 476, Appl |
| 43 | 332 | 23.2 | 253 | 4 | US-10-156-136-35 | Sequence 35, Appl |
| 44 | 332 | 23.2 | 253 | 6 | US-11-041-419-35 | Sequence 35, Appl |
| 45 | 332 | 23.2 | 282 | 3 | US-09-925-301-1234 | Sequence 1234, Appl |

ALIGNMENTS

RESULT 1
US-09-155-008-3
; Sequence 3, Application US/09155008
; Patent No. US20020165378A1
; GENERAL INFORMATION:
; APPLICANT: Kato, Seishi
; APPLICANT: Sekine, Shingo
; APPLICANT: Yamaguchi, Tomoko
; TITLE OF INVENTION: Human Membrane Antigen TM4 Superfamily Protein and DNA
; FILE REFERENCE: Encoding This Protein
; FILE REFERENCE: GI 6702PCT-US
; CURRENT APPLICATION NUMBER: US/09/155,008
; CURRENT FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 3
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-155-008-3

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Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 3 Gaps: 0

US-10-608-388A-1 (1-759) x US-09-155-008-3 (1-253)

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Db 1 MetGlyGlnCysGlyIleThrSerGlyThrValLeuValPheLeuAnLeuIlePhe 20

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QY 121 TATGACCACTCTCTTTGAAGATGTACACGCTCATCCCTGCTGTAGTGTATGATCATGCTGTA 180
DB 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleAlaVal 60
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DB 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
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QY 301 GTGGTTTGGGATATGTTTACAGAGCAAAAGTGGAAATGAGGTTGATCGCAGCATTCAG 360
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QY 361 AAAGTGTATAGACCTACATGGAACCAACCTGATGCTGTAGCCGGGCTATTGATTTAT 420
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QY 661 GCTATTACAGCTCTGGGATGCTGTGCTTGTGCTATGCTGTGCTGAGAGGAGTATGAGAT 720
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RESULT 2

US-09-983-000A-18
; Sequence 18, Application US/09983000A
; Publication No. US20030118585A1
; GENERAL INFORMATION:
; APPLICANT: AGY Therapeutics
; APPLICANT: Melcher, Thorsten
; APPLICANT: Mueller, Sabine
; APPLICANT: Chin, Daniel
; TITLE OF INVENTION: USE OF PROTEIN BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUALIZ
; FILE REFERENCE: 263/180 -- PEGASMAN -- AGY
; CURRENT APPLICATION NUMBER: US/09/983,000A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(11)
; OTHER INFORMATION: Cytoplasmic (Potential)
; NAME/KEY: Gene

; LOCATION: (1)..(253)
; OTHER INFORMATION: Tetraspanin-3
; NAME/KEY: TRANSMEM
; LOCATION: (12)..(32)
; OTHER INFORMATION: Potential
; NAME/KEY: DOMAIN
; LOCATION: (33)..(50)
; OTHER INFORMATION: Extracellular (Potential)
; NAME/KEY: TRANSMEM
; LOCATION: (51)..(71)
; OTHER INFORMATION: Potential
; NAME/KEY: DOMAIN
; LOCATION: (72)..(85)
; OTHER INFORMATION: Cytoplasmic (potential)
; NAME/KEY: TRANSMEM
; LOCATION: (86)..(106)
; OTHER INFORMATION: Potential
; NAME/KEY: DOMAIN
; LOCATION: (107)..(212)
; OTHER INFORMATION: Extracellular (potential)
; NAME/KEY: TRANSMEM
; LOCATION: (213)..(233)
; OTHER INFORMATION: Potential
; NAME/KEY: DOMAIN
; LOCATION: (234)..(253)
; OTHER INFORMATION: Cytoplasmic (potential)
; NAME/KEY: CARBOHYD
; LOCATION: (127)..(127)
; OTHER INFORMATION: N-linked (GLCNAC...) (potential)
; NAME/KEY: CARBOHYD
; LOCATION: (152)..(152)
; OTHER INFORMATION: N-linked (GLCNAC...) (potential)
; NAME/KEY: CARBOHYD
; LOCATION: (167)..(167)
; OTHER INFORMATION: N-linked (GLCNAC...) (potential)
; NAME/KEY: CARBOHYD
; LOCATION: (183)..(183)
; OTHER INFORMATION: N-linked (GLCNAC...) (potential)
US-09-983-000A-18

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Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 3 Gaps: 0

US-10-608-388A-1 (1-759) x US-09-983-000A-18 (1-253)

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DB 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
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; Sequence 66, Application US/10223084
; Publication No. US20030105012A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C5
; CURRENT APPLICATION NUMBER: US/10/223,084
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 66
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-084-66

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Score: 1336.00
Length: 253
Matches: 253
Conservative: 0
Percent Similarity: 100.0%
Mismatches: 0
Best Local Similarity: 100.0%
Indels: 0
Query Match: 93.5%
Gaps: 4
DB:

US-10-608-388a-1 (1-759) x US-10-223-084-66 (1-253)

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Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
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Db 241 ProAlaTyrGluLeuLeuIleThrGlyThrTyrAla 253

RESULT 5
US-10-223-088-66
; Sequence 66, Application US/10223088
; Publication No. US20030105012A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C6
; CURRENT APPLICATION NUMBER: US/10/223,088
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
```

PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 66
LENGTH: 253
TYPE: PRT
ORGANISM: Homo sapiens
US-10-223-088-66

Alignment Scores:
Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 4 Gaps: 0

US-10-608-388A-1 (1-759) x US-10-223-088-66 (1-253)

QY 1 ATGGGCGAGTGGCGCATCCTCTCAAGACCGTGGTGGTCTTCTCAACCTCATCTTC 60
DB 1 MetGlyGlnCysGlyLeuThrSerSerLysThrValLeuValPheLeuLeuLeuPhe 20

QY 61 TGGGGGCGAGCTGGCAATTTATGCTATGTGGAGCTATGCTTTCATCACTTATGATGAC 120
DB 21 TrpGlyAlaAlaGlyLeuLeuCysTyrValGlyAlaTyrValPheLeuThrTyrAspAsp 40

QY 121 TATGACCACTTCTTCAAGATGTACAGCTCATCCCTGCTGTGCCACAATCCGGAAAGTCGC 240
DB 41 TyrAspHisPhePheGluAspValTyrThrLeuLeuProAlaValValLeuLeuAlaVal 60

QY 181 GGAGCCCTGCTTTTCATCTGGGCTAATGGCTGTGCTGCCACAATCCGGAAAGTCGC 240
DB 61 GlyAlaLeuLeuPheLeuLeuGlyLeuLeuGlyCysCysAlaThrLeuArgGluSerArg 80

QY 241 TGTGGACTTGGCACTGTTTGTATCATCTGCTCTTGGTGGTGGTGGTGGTGGTGGTGGT 300
DB 81 CysGlyLeuAlaThrPheValLeuLeuLeuLeuLeuValPheValThrGluValValVal 100

QY 301 GTGGTTTGGGATATTTTACAGAGCAGAAAGTGGAAATGAGGTTGATCGCAGCATTCAG 360
DB 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120

QY 361 AAAGTCTATAAGACCTTACAAATGAACCAACCTGATGCTAGCCGGCTATTGATTAT 420
DB 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaSerArgAlaLeuAspTyr 140

QY 421 GTACAGAGCAGCTGATTTGTGGAATTCACAACTACTCATCTGAGTGGGAAATACAGAT 480
DB 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160

QY 481 TGGTTCAAGAAACCAACCAAGAGTGGCTTCTTGTGCTGGCAGAGACTGCCAGC 540
DB 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180

QY 541 AATTGTAATGGCAGCTGGCCACCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
DB 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200

QY 601 GTAGTGAAGAGCTACAAGAAATCATGATGCGATGTGCTGGGCCCGCACTGGCATTTGCA 660
DB 201 ValValLysLysLeuGlnGluLeuMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220

QY 661 GCTATTACGCTCTGGGCATGCTGTGCTTGCATCGTGTGGCAGAGGCTAGAGAT 720
DB 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgasp 240

QY 721 CTGCTTACGAGCTCTCATCATCTGCGGGAACCTATGCA 759
DB 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

RESULT 6

US-10-223-090-66
Sequence 66, Application US/10223090
Publication No. US20030105013A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P. Mickey
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235P1C2
CURRENT APPLICATION NUMBER: US/10/223,090
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 10/081,056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 66
LENGTH: 253
TYPE: PRT
ORGANISM: Homo sapiens
US-10-223-090-66

Alignment Scores:
Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 4 Gaps: 0

US-10-608-388A-1 (1-759) x US-10-223-090-66 (1-253)

QY 1 ATGGGCGAGTGGCGCATCCTCTCAAGACCGTGGTGGTCTTCTCAACCTCATCTTC 60

Db 1 MetGlyGlnCysGlyLeuThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
Qy 61 TGGGGGGGAGCTGGCATTTTATGCTATGTGGAGGCTATGCTTCATCATCTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
Qy 121 TATGACCACTCTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTGTATCATCATGCTGTA 180
Db 41 TyrAspHisPheGluAspValTyrThrLeuIleProAlaValIleIleAlaVal 60
Qy 181 GGAGCCCTGCTTTTCATCATTTGGCTAATTTGGCTGCTGTGCCACAACTCGGGAAGTGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
Qy 241 TGTGACTTGGCAGCTTTGTGTATCTCTGCTCTCTGCTTTTGTTCACAGAAGTTGTGTA 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
Qy 301 GTGCTTTGGGATATGTTTACAGACAAAGGTGGAATGAGTTGTGATCGCAGCATTCAG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
Qy 361 AAAGTGTATAAGACTACAACTGAAGCAACCTGCTGCTGTAGTGTGCTGCTGCTGCTGCTAT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
Qy 421 GTACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTyrGluAsnThrAsp 160
Qy 481 TGGTTCAAGAAACCAAAACAGAGTCTCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
Qy 541 AATTGTAATGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
Qy 601 GTAGTGAAGAGCTACAAGAATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 201 ValValLysLysLeuGlnGluIleMetMethHisValIleTyrAlaAlaLeuAlaPheAla 220
Qy 661 GCTATTGAGCTGCTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 240
Qy 721 CCTGCTTACGAGCTCTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

FILE REFERENCE: P323SP1C4
CURRENT APPLICATION NUMBER: US/10/223,087
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 10/081,056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/230,978
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/232,887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 09/664,610
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/242,922
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 09/709,238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/30952
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/747,259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/767,609
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 09/796,498
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06666
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: US 09/802,706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/808,689
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 09/816,744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 09/828,366
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 09/854,208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/854,280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/866,034
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/US01/17092
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/870,574
PRIOR FILING DATE: 2001-05-30

RESULT 7

US-10-223-087-66
Sequence 66, Application US/10223087

Publication No. US20030109438A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Ferrara, Napoleone

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Marsters, Scot A.

APPLICANT: Pan, James

APPLICANT: Stephan, Jean-Philippe P.

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Williams, P. Mickey

APPLICANT: Ye, Weilan

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS

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; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 66
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-087-66

Alignment Scores:
Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 4 Gaps: 0

US-10-608-388A-1 (1-759) x US-10-223-087-66 (1-253)
QY 1 ATGGCCAGTGGGCATCACTCTCCAGACCGTGTCTTCTCAACCTCATCTTC 60
DB 1 MetGlycylcysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
QY 61 TGGGGGCGAGTGGCATTTATGCTATGTGGGACCTATGCTTTCATCATATGATGAC 120
DB 21 TrpGlyAlaAlaGlyIleLeuGlySerValGlyAlaIleValPheIleThrThrAsp 40
QY 121 TATGACCACTTCTTTGAAGATGTGTACACGCTCATCTCTGTCTGTAGTGTATCATGCTGTA 180
DB 41 TyrAspHisPhePheGluAspValTy-ThrLeuIleProAlaValValIleAlaVal 60
QY 181 GGAGCCCTGCTTTTCATCTATGGGCTAATTGGCTGTCTGTGCACAAATCCGGGAAGTCGC 240
DB 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
QY 241 TGTGGACTTCCAGCTTGTTCATCATCTCTCTCTGTCTTGTCTTGTGTGTGTGTGTGTGTGT 300
DB 81 CysGlyLeuAlaThrPheValIleIleLeuLeuLeuValPheValThrGluValValVal 100
QY 301 GTGGTTTGGGATATGTTTACAGACAAAGGTGAAATGAGGTTGATCGCAGCATTCAG 360
DB 101 ValValLeuGlyTyValTyValTyValTyValTyValTyValTyValTyValTyValTyVal 120
QY 361 AAAGTGTATGAACCTACAAATGGAACCAACCTGATCTCTAGCCGGGCTATTGATTAT 420
DB 121 LysValTyIleThrTyAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGACAGCTGCTGCTGTGGATTACAACTACTCAGACTGCGGAAATACAGAT 480
DB 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
QY 481 TGTGTTCAAGAAACCAAAACACAGAGTGTCCCTCTTACGCTGTGCAGAGACTGCCAGC 540
DB 161 TrpPheIleGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATCGGAGCTGGCCCACTCTCCAGCTCTATGCTGAGGGGTGTAGGCTCTTA 600
DB 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAGCTACAGAAATCATCATCATGCTGATCTGGCCGACCTGGCATTTGCA 660
DB 201 ValValIleLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
QY 661 GCTATTACGCTGGGCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
DB 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20

Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 240
QY 721 CCTGCTTACGAGCTCTCTCATCTCACTGCGGGAACCTATGCA 759
DB 241 ProAlaTyrGlnLeuLeuIleThrGlyGlyThrTyrAla 253

RESULT 8
US-10-223-083-66
; Sequence 66 Application US/10223083
; Publication No. US20030119112A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PIC8
; CURRENT APPLICATION NUMBER: US/10/223,083
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 66
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-083-66

Alignment Scores:
Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 4 Gaps: 0

US-10-608-388A-1 (1-759) x US-10-223-083-66 (1-253)
QY 1 ATGGCCAGTGGGCATCACTCTCCAGACCGTGTCTTCTCAACCTCATCTTC 60
DB 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
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QY 61 TGGGGGCGAGCTGGCATTTTATGCTATGTGGGAGCTATGCTTTCATCACTATGATGAC 120
DB 21 TrpGlyAlaAlaGlyLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACCACTTCTTTGAAGATGTGTACAGCTCATCTCTGCTGTAGTATGATCATGCTGTA 180
DB 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleAlaVal 60
QY 181 GGAGCCCTGCTTTTCATCATTTGGGCTAATGGCTGCTGCCACATCGGGAAGTGC 240
DB 61 GlyAlaLeuLeuPheIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
QY 241 TGTGACTTGCACCTTTGTATCATCTCTGCTCTCTGCTTTGTGTCACAGAAAGTGTGCTA 300
DB 81 CysGlyLeuAlaThrPheValIleLeuLeuValPheValThrGluValValVal 100
QY 301 CTGCTTTGGGATATGTTTACAGACAAAGGTGGAATGAGTTGATCGGAGCATTCAG 360
DB 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
QY 361 AAAGTGTATAGACCTACATGGAACCAACCTGATGCTGTAGCGGGCTATTGATTAT 420
DB 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGACAGCTGCATTGTTGTGGAATTCACAACTACTCAGACTGGGAAATACAGAT 480
DB 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTyrPGLuAsnThrAsp 160
QY 481 TGGTTCAAAGAAACCAAAACAGAGTGTCCCTCTTATGCTGTGACAGAGACTGCCAGC 540
DB 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATGGAGCTGGCCACCCCTCCGACCTCTATGCTGAGGGGTGTGAGCTCTA 600
DB 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAGCTACAGAAATCATGATGATGATGCTGGGCGCACTGGCATTTGCA 660
DB 201 ValValLysLysLeuGlnGluIleMetHisValIleThrPalaAlaLeuAlaPheAla 220
QY 661 GCTATTACAGCTCTGGGATGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 240
QY 721 CTGCTTACAGAGCTCTCATCATCTGGGGAACCTATGCA 759
DB 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

RESULT 9

US-10-223-089-66
; Sequence 66, Application US/10223089
; Publication No. US20030125521A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C9
; CURRENT APPLICATION NUMBER: US/10/223, 089
; CURRENT FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 66
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-089-66
Alignment Scores:
Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 4 Gaps: 0
US-10-608-388a-1 (1-759) x US-10-223-089-66 (1-253)
QY 1 ATGGGCGAGCTGGGATCATCTCTCAAGACCTGCTGCTCTTCTCAACCTCATCTTC 60
DB 1 MetGlyGlnCysGlyIleThrSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
QY 61 TGGGGGCGAGCTGGCATTTTATGCTATGTGGGAGCTATGCTTTCATCACTATGATGAC 120
DB 21 TrpGlyAlaAlaGlyLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACCACTTCTTTGAAGATGTGTACAGCTCATCTCTGCTGTAGTATGATCATGCTGTA 180
DB 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleAlaVal 60
QY 181 GGAGCCCTGCTTTTCATCATTTGGGCTAATGGCTGCTGCCACATCGGGAAGTGC 240
DB 61 GlyAlaLeuLeuPheIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
QY 241 TGTGACTTGCACCTTTGTATCATCTCTGCTCTCTGCTTTGTGTCACAGAAAGTGTGCTA 300
DB 81 CysGlyLeuAlaThrPheValIleLeuLeuValPheValThrGluValValVal 100
QY 301 CTGCTTTGGGATATGTTTACAGACAAAGGTGGAATGAGTTGATCGGAGCATTCAG 360
DB 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
QY 361 AAAGTGTATAGACCTACATGGAACCAACCTGATGCTGTAGCGGGCTATTGATTAT 420
DB 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGACAGCTGCATTGTTGTGGAATTCACAACTACTCAGACTGGGAAATACAGAT 480
DB 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTyrPGLuAsnThrAsp 160
QY 481 TGGTTCAAAGAAACCAAAACAGAGTGTCCCTCTTATGCTGTGACAGAGACTGCCAGC 540
DB 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180

APPLICANT: Pan, James
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P. Mickey
APPLICANT: Ye, Weilan
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235R1C3
CURRENT APPLICATION NUMBER: US/10/223,082
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 10/081,056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 66
LENGTH: 253
TYPE: PRT
ORGANISM: Homo sapiens
US-10-223-082-66

Alignment Scores:
Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 4 Gaps: 0

US-10-608-388A-1 (1-759) x US-10-223-082-66 (1-253)

QY 1 ATGGGCCAGTGGCGATCCTCCAGACCGTGGTCTTCTCAACCTCATCTTC 60
DB 1 MetGlyGlnCysGlyIleThrSerLysThrValLeuValPheLeuAsnLeuIlePhe 20

QY 61 TGGGGGGCAGCTGGCATTTTATGCTATGTGGGAGCTATGCTTCATCACTTATGATGAC 120
DB 21 trpGlyAlaAlaGlyIleLeuLeuCysTyrValGlyAlaTyrValPheIleThrThrAsp 40

QY 121 TATGACCACTCTTTCAAGATGTACACGCTCATCCCTGCTGTAGTATCATAGCTGTA 180
DB 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleIleAlaVal 60

QY 181 GGAGCCCTGCTTTTTCATCATTTGGCTAATGGCTGCTGTCACCAATCCGGAAAGTCGC 240
DB 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleIleGluSerArg 80

QY 241 TGTGGACTTGGCAGCTTGTCTATCATCCGCTCTTGGTGTGTGTGTGTGTGTGTGTGT 300
DB 81 CysGlyLeuAlaThrPheValIleIleLeuLeuLeuValPheValThrGluValValVal 100

QY 301 GTGGTTTGGGATGATTTTACAGACAAAGGTGGAAATGAGGTTGATCGCAGCATTCAG 360
DB 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120

QY 361 AAAGTGATTAAGACCTACAATGGAACCAACCTGCTGCTAGCCGGCTATTGATTAT 420
DB 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaLysArgAlaIleAspTyr 140

QY 421 GTACAGACAGCTGCATTTGTTGGAAATTCACAACCTACTCAGACTGGGAAATACAGAT 480
DB 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160

QY 481 TGGTTTCAAGAAACCAAAACACAGAGTGTCCCTCTTAGCTCTGCAGAGAGACTGCCAGC 540
DB 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180

QY 541 AATTGTAATGGCAGCTGGCCACCCTTCCGACCTCTATGCTGAGGGGTGAGGCTCTA 600
DB 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200

QY 601 GTAGTGAAGAGCTACAAGAANTCATGATGATGATCTGCGCGGCACTGGCATTTGCA 560
DB 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220

QY 661 GCTATTTCAGCTGCTGGGCATGCTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 240

QY 721 CCTGCTTACGAGCTCTCATCATCTGCGGGAACCTATGCA 759
DB 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

RESULT 12
US-10-305-654-66
Sequence 66, Application US/10305654
Publication No. US20030224984A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hans-Peter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, J.
APPLICANT: Paoni, N. F.
APPLICANT: Stephan, J-P. F.
APPLICANT: Watanabe, C.K.
APPLICANT: Wood, W.I.
APPLICANT: Williams, P.M.
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235R1C1
CURRENT APPLICATION NUMBER: US/10/305,654
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 66
LENGTH: 253
TYPE: PRT
ORGANISM: Homosapiens
US-10-305-654-66

Alignment Scores:
Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 4 Gaps: 0

US-10-608-388A-1 (1-759) x US-10-305-654-66 (1-253)

QY 1 ATGGGCCAGTGGCGATCCTCCAGACCGTGGTCTTCTCAACCTCATCTTC 60
DB 1 ATGGGCCAGTGGCGATCCTCCAGACCGTGGTCTTCTCAACCTCATCTTC 60

Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAasnLeuIlePhe 20
QY 61 TGGGGGCGAGCTGCATTATGCTATGCTGGAGCCCTATCTTCATCATCTTATGATGAC 120
Db 21 TrpGlyAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACCACTTCTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTCATCATGCTGTA 180
Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValIleIleAlaVal 60
QY 181 GGAGCCCTGCTTTTCATCATTTGGGCTAATTTGGCTGTGTGTCACCAATCCGGGAAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysAlaThrIleArgGluSerArg 80
QY 241 TGTGACCTTGCACGTTTGTTCATCATCTGCTCTTGGTTTGTTCACAGAAGTTGTTGTA 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValIleVal 100
QY 301 GTGTTTTGGGATATGTTTACAGACAAAGGTGGAATGAGTTGATCGCAGCATTCAG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAasnGluValAspArgSerIleGln 120
QY 361 AAGTGTATAGACCTACATGGAACCAACCTGATGCTGCTAGCCGGGCTATTGATAT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGACAGCTGCATTGTTGTGGAATTCACAACTACTCAGACTGCGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
QY 481 TGGTTCAAGAAACCAAAACACAGAGTGCCTCTTAGCTGCTGCAGAGAGACTGCCAGC 540
Db 161 TrpPheLysGlnThrLysAasnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATGGCAGCTGGCCCACTTCGACCTTCGACCTGATGCTGAGGGGTGTGAGGCTTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAGCTACAGAAATCATGATCATGCTGATCTGGCCGCACTGGCATTGCA 660
Db 201 ValValLysLysLeuGlnGluMetHisValIleTrpAlaAlaLeuAlaPheAla 220
QY 661 GCTATTGAGCTGCTGGCAGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgAspArgAsp 240
QY 721 CTRGCTTACAGCTCTTCATCATCTGCGGCAACCTATGCA 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

RESULT 13

US-10-081-056-66

; Sequence 66, Application US/10081056

; Publication No. US20040043927A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Marsters, Scot A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Ye, Weilan

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS

FILE REFERENCE: P3235PIC1
; CURRENT APPLICATION NUMBER: US/10/081,056
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/230,978
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/000,000
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/664,610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/242,922
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/709,238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30952
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/767,609
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 09/796,498
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/802,706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/808,689
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 09/828,366
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/854,280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/866,034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/870,574
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30

;; PRIOR APPLICATION NUMBER: PCT/US01/17800
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: PCT/US01/19692
;; PRIOR FILING DATE: 2001-06-20
;; PRIOR APPLICATION NUMBER: PCT/US01/00000
;; PRIOR FILING DATE: 2001-06-28
;; NUMBER OF SEQ ID NOS: 383
;; SEQ ID NO 66
;; LENGTH: 253
;; TYPE: PRT
;; ORGANISM: Homosapiens
US-10-081-056-66

Alignment Scores:
Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 4 Gaps: 0

US-10-608-388A-1 (1-759) x US-10-081-056-66 (1-253)

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| Qy | 1 | ATGGCCAGTGGGACATCACTCTCCAGACCGTGTCTTTCTCAACCTCATCTTC | 60 |
| Db | 1 | MetGlyGlnCysGlyLeuThrSerSerValLeuValPheLeuAsnLeuPhe | 20 |
| Qy | 61 | TGGGGGAGCTGGGATTTATGCTATGTTGGAGCTATCTTCATCATCTATGATGAC | 120 |
| Db | 21 | TrpGlyAlaAlaGlyLeuLeuCysTyrValGlyAlaTyrValPheIleThrTyrAsp | 40 |
| Qy | 121 | TATGACCACTCTTTGAGATGTGTACAGCTCATCCCTGCTGTAGTATCATCTGTA | 180 |
| Db | 41 | TyrAspHisPheGluAspValTyrThrLeuIleProAlaValIleIleIleVal | 60 |
| Qy | 181 | GGAGCCCTGCTTTTCATCATCTGGGCTAATTGCTGTGTGCCACATCCGGAAAGTCGC | 240 |
| Db | 61 | GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysAlaThrIleArgGluSerArg | 80 |
| Qy | 241 | TGTGACCTGGCAGCTTTGTGCTATCTCTGCTCTTGGTTTGTTCACAGAAGTTGTTGA | 300 |
| Db | 81 | CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValVal | 100 |
| Qy | 301 | GTGTTTGGGATATGTTTACAGACAAAGTGGAAATGAGTTGATCGCAGCATTCAG | 360 |
| Db | 101 | ValValLeuGlyTyrValTyrArgAlaValGluAsnGluValAspArgSerIleGln | 120 |
| Qy | 361 | AAAGTGATTAAGACCTACAATGGAACCACTGCTGTGTAGCTGCTGCTGCTATTGATTAT | 420 |
| Db | 121 | LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr | 140 |
| Qy | 421 | GTACAGACAGCTGCTGTTGTGGATTCACACTACTCAGACTGGGAAATACAGAT | 480 |
| Db | 141 | ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp | 160 |
| Qy | 481 | TGTTTCAAGAACCAAAACAGAGTGTCCCTCTAGCTGTGTGAGAGACTGCCAGC | 540 |
| Db | 161 | TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysArgGluThrAlaSer | 180 |
| Qy | 541 | AATTGTATGTCAGCTGCGCCACCTCTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA | 600 |
| Db | 181 | AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu | 200 |
| Qy | 601 | GTAGTGAAGAACTACAAGAAATCATGATGATGTGATCTGGGCGCGACTGGCATTTGA | 660 |
| Db | 201 | ValValLysLysGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla | 220 |
| Qy | 661 | GCTATTACGCTCTGGGATGTGTGCTTCATGCTGTGTGAGAGGAGTAGAGAT | 720 |
| Db | 221 | AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp | 240 |
| Qy | 721 | CCTGCTTACGAGCTCTCATCTACTGGCGAACTATGCA | 759 |

Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253
RESULT 14
US-10-652-981-18
;; Sequence 18, Application US/10652981
;; Publication No. US20050074400A1
;; GENERAL INFORMATION:
;; APPLICANT: AGY Therapeutics
;; APPLICANT: Melcher, Thorsten
;; APPLICANT: Mueller, Sabine
;; APPLICANT: Chin, Daniel
;; TITLE OF INVENTION: USE OF PROTEIN BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUAL
;; FILE REFERENCE: 263/180 -- Peagleman -- AGY
;; CURRENT APPLICATION NUMBER: US/10/652,981
;; CURRENT FILING DATE: 2003-08-28
;; PRIOR APPLICATION NUMBER: US/09/983,000A
;; PRIOR FILING DATE: 2001-10-17
;; NUMBER OF SEQ ID NOS: 35
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 18
;; LENGTH: 253
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURES:
;; NAME/KEY: DOMAIN
;; LOCATION: (1)..(11)
;; OTHER INFORMATION: Cytoplasmic (Potential)
;; FEATURE:
;; NAME/KEY: Gene
;; LOCATION: (1)..(253)
;; OTHER INFORMATION: Tetraspanin-3
;; FEATURE:
;; NAME/KEY: TRANSMEM
;; LOCATION: (12)..(32)
;; OTHER INFORMATION: Potential
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (33)..(50)
;; OTHER INFORMATION: Extracellular (Potential)
;; FEATURE:
;; NAME/KEY: TRANSMEM
;; LOCATION: (51)..(71)
;; OTHER INFORMATION: Potential
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (72)..(85)
;; OTHER INFORMATION: Cytoplasmic (potential)
;; FEATURE:
;; NAME/KEY: TRANSMEM
;; LOCATION: (86)..(106)
;; OTHER INFORMATION: Potential
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (107)..(212)
;; OTHER INFORMATION: Extracellular (potential)
;; FEATURE:
;; NAME/KEY: TRANSMEM
;; LOCATION: (213)..(233)
;; OTHER INFORMATION: Potential
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (234)..(253)
;; OTHER INFORMATION: Cytoplasmic (potential)
;; FEATURE:
;; NAME/KEY: CARBOHYD
;; LOCATION: (127)..(127)
;; OTHER INFORMATION: N-linked (GLCNAC...) (potential)
;; FEATURE:
;; NAME/KEY: CARBOHYD
;; LOCATION: (152)..(152)
;; OTHER INFORMATION: N-linked (GLCNAC...) (potential)
;; FEATURE:

; NAME/KEY: CARBOHYD
; LOCATION: (167)...(167)
; OTHER INFORMATION: N-linked (GLCNAC...) (potential)
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (183)...(183)
; OTHER INFORMATION: N-linked (GLCNAC...) (potential)
US-10-652-981-18

Alignment Scores:
Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 5 Gaps: 0

US-10-608-388A-1 (1-759) x US-10-652-981-18 (1-253)

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QY 1 ATGGGCCAGTCGGGCATCACCTCTCCAAAGACCGTGTGCTTTCTCAACCTCATCTTC 60
DB 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
QY 61 TGGGGGCGAGCTGGCATTATATGCTATGTTGGAGCCTATGCTTTTCATCATTATGATGAC 120
DB 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACACACTCTTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTATCATAGCTGTA 180
DB 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValIleAlaVal 60
QY 181 GGAGCCCTGCTTTTCATCATTGGGCTAATTTGGCTGTGTGCTGTCACAAATCCGGAAAGTCGC 240
DB 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysAlaThrIleAspGluSerArg 80
QY 241 TGTGGACTTGCCAGCTGCTGTCATCATCTGCTCTTGTGTTTGTGCACAGAAGTTGTTGTA 300
DB 81 CysGlyLeuAlaThrPheValIleLeuLeuValPheValThrGluValVal 100
QY 301 GTGGTTTGGGATATGTTTACAGAACAAAGTGGAATAGAGTTGATCCGAGCAATTCAG 360
DB 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
QY 361 AAGTGTATAGACCTACAAAGAACCAACCTGCTGCTAGCTGCTAGCCGGCTATTGATTAT 420
DB 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGACAGCTGCAATTTGTTGGAAATTCACAACTACTCAGACTGGGAAATATACAGAT 480
DB 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
QY 481 TGGTTCAAAGAAACCAAAACCAAGTGCGTCCCTCTTAGCTGCTCAGAGAGACTGCCAGC 540
DB 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATGCGACCTGGCCACCTTCCGACCTCTATGCTAGGGGTGTGAGGCTCTA 600
DB 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAGCTACAAAGAAATCATGATGATGTGATGCTGGGCGGCACTGGCATTTCGA 660
DB 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
QY 661 GCTATTGCTGGGATGCTGTGCTGTGATCGTGTGATCGTGTGTCGAGAGAGTAGAT 720
DB 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
QY 721 CCTGCTTACAGCTCCCTCATCCTGCGGACCTATGCA 759
DB 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253
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RESULT 15

US-10-631-467-635

; Sequence 635, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genex Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructiv
; FILE OF INVENTION: disease
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 635
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-635

Alignment Scores:
Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 5 Gaps: 0

US-10-608-388A-1 (1-759) x US-10-631-467-635 (1-253)

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QY 1 ATGGGCCAGTCGGGCATCACCTCTCCAAAGACCGTGTGCTTTCTCAACCTCATCTTC 60
DB 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
QY 61 TGGGGGCGAGCTGGCATTATATGCTATGTTGGAGCCTATGCTTTTCATCATTATGATGAC 120
DB 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACACACTCTTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTATCATAGCTGTA 180
DB 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValIleAlaVal 60
QY 181 GGAGCCCTGCTTTTCATCATTGGGCTAATTTGGCTGTGTGCTGTCACAAATCCGGAAAGTCGC 240
DB 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysAlaThrIleAspGluSerArg 80
QY 241 TGTGGACTTGCCAGCTGCTGTCATCATCTGCTCTTGTGTTTGTGCACAGAAGTTGTTGTA 300
DB 81 CysGlyLeuAlaThrPheValIleLeuLeuValPheValThrGluValVal 100
QY 301 GTGGTTTGGGATATGTTTACAGAACAAAGTGGAATAGAGTTGATCCGAGCAATTCAG 360
DB 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
QY 361 AAGTGTATAGACCTACAAAGAACCAACCTGCTGCTAGCTGCTAGCCGGCTATTGATTAT 420
DB 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGACAGCTGCAATTTGTTGGAAATTCACAACTACTCAGACTGGGAAATATACAGAT 480
DB 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
QY 481 TGGTTCAAAGAAACCAAAACCAAGTGCGTCCCTCTTAGCTGCTCAGAGAGACTGCCAGC 540
DB 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATGCGACCTGGCCACCTTCCGACCTCTATGCTAGGGGTGTGAGGCTCTA 600
DB 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAGCTACAAAGAAATCATGATGATGTGATGCTGGGCGGCACTGGCATTTCGA 660
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Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrrAlaAlaLeuAlaPheAla 220
QY 661 GCTATTTCAGCTGCTGGGCATGCTGTGCTTGCATCGTCTTGTGCGAAGGAGTACAGAT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 240
QY 721 CCTGCTTACGAGCTCCTCATCTGCGGGAACCTATGCA 759
Db 241 ProAlaIyr-GluLeuLeuIleThrGlyThrTyrAla 253

Search completed: April 4, 2006, 21:55:23
Job time : 159 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, **us-10-608-388a-1.n2p.rag**

Run on: April 4, 2006, 21:17:49 ; Search time 32.2 Seconds
(without alignments)
2071.357 Million cell updates/sec

Title: US-10-608-388a-1

Perfect score: 1429

Sequence: 1 atggggcagcgccgcatcac.....tcactggcggaacctatgca 759

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSSWEB/spool/US10608388/runat_04042006_150646_14026/app_query.fasta 1
-DB=A_Geneseq -QWMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcr -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02p
-USER=US10608388 @CGN_1_1_348_ornat_04042006_150646_14026 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6 -FCGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 1336 | 93.5 | 253 | 2 AAW7333 | AAW7333 Human mem |
| 2 | 1336 | 93.5 | 253 | 2 AAW74469 | AAW74469 HP00966 p |
| 3 | 1336 | 93.5 | 253 | 4 AAB92850 | AAB92850 Human pro |
| 4 | 1336 | 93.5 | 253 | 4 AAB92830 | AAB92830 Human pro |
| 5 | 1336 | 93.5 | 253 | 5 ABB84849 | ABB84849 Human PRO |
| 6 | 1336 | 93.5 | 253 | 5 ABB95455 | ABB95455 Human ang |
| 7 | 1336 | 93.5 | 253 | 6 AAE30341 | AAE30341 Human tet |
| 8 | 1336 | 93.5 | 253 | 7 ADD14059 | ADD14059 Human src |
| 9 | 1336 | 93.5 | 253 | 7 ADD10355 | ADD10355 Human sec |

| | | | | | |
|----|-------|------|-----|------------|--------------------|
| 10 | 1336 | 93.5 | 253 | 7 ADD11315 | ADD11315 Human sec |
| 11 | 1336 | 93.5 | 253 | 7 ADD37108 | ADD37108 Human sec |
| 12 | 1336 | 93.5 | 253 | 7 ADD45736 | ADD45736 Human pro |
| 13 | 1336 | 93.5 | 253 | 8 ADE41316 | ADE41316 Human sec |
| 14 | 1336 | 93.5 | 253 | 8 ADH43499 | ADH43499 Human PRO |
| 15 | 1336 | 93.5 | 253 | 8 ADJ75383 | ADJ75383 Marker ge |
| 16 | 1336 | 93.5 | 253 | 8 ADK82844 | ADK82844 Human PRO |
| 17 | 1336 | 93.5 | 253 | 8 ABM81655 | ABM81655 Tumour-as |
| 18 | 1336 | 93.5 | 253 | 8 ADP23080 | ADP23080 PRO polyp |
| 19 | 1336 | 93.5 | 253 | 8 ADP23078 | ADP23078 PRO polyp |
| 20 | 1332 | 93.2 | 253 | 2 AAW61621 | AAW61621 Clone HLT |
| 21 | 1332 | 93.2 | 253 | 7 ABW01503 | ABW01503 Human rec |
| 22 | 1329 | 93.0 | 253 | 4 AAB92827 | AAB92827 Human pro |
| 23 | 1322 | 92.5 | 253 | 9 AEB98434 | AEB98434 Human HLT |
| 24 | 1301 | 91.0 | 253 | 8 AD45735 | AD45735 Rat Prote |
| 25 | 1301 | 91.0 | 253 | 8 ADJ76179 | ADJ76179 Marker ge |
| 26 | 1300 | 91.0 | 252 | 3 AAY87784 | AAY87784 Human TM4 |
| 27 | 1300 | 91.0 | 252 | 7 ABW02029 | ABW02029 Human tra |
| 28 | 1300 | 91.0 | 252 | 7 ADG47652 | ADG47652 Human TM4 |
| 29 | 624 | 43.7 | 124 | 2 AAY12214 | AAY12214 Human 5' |
| 30 | 515 | 36.0 | 119 | 4 AAO07140 | AAO07140 Human pol |
| 31 | 384 | 26.9 | 254 | 9 ADY54293 | ADY54293 Human 232 |
| 32 | 352 | 24.6 | 166 | 5 ABB78818 | ABB78818 Tetraepan |
| 33 | 343.5 | 24.0 | 244 | 7 ABW01517 | ABW01517 Protein # |
| 34 | 343.5 | 24.0 | 244 | 8 ADK60220 | ADK60220 Angiogene |
| 35 | 343.5 | 24.0 | 244 | 8 ADK60521 | ADK60521 Angiogene |
| 36 | 343.5 | 24.0 | 244 | 8 ADN05840 | ADN05840 Antipsori |
| 37 | 343.5 | 24.0 | 244 | 8 ADP73144 | ADP73144 Angiogene |
| 38 | 343.5 | 24.0 | 244 | 9 AEB98448 | AEB98448 Human TAL |
| 39 | 343.5 | 24.0 | 249 | 8 ADO55160 | ADO55160 Protein # |
| 40 | 342 | 23.9 | 253 | 7 ADD48735 | ADD48735 Rat Prote |
| 41 | 340 | 23.8 | 253 | 3 AAY69779 | AAY69779 Mouse tum |
| 42 | 336 | 23.5 | 253 | 5 AAO18875 | AAO18875 Simian CD |
| 43 | 334.5 | 23.4 | 244 | 7 ADS85224 | ADS85224 Mouse cel |
| 44 | 333.5 | 23.3 | 245 | 2 AAW61620 | AAW61620 Clone HSB |
| 45 | 333.5 | 23.3 | 245 | 2 AAY28677 | AAY28677 Human bxl |

ALIGNMENTS

RESULT 1
AAW27333
ID AAW27333 standard; protein; 253 AA.

AC AAW27333;
XX
XX 16-JAN-1998 (first entry)
XX
XX Human membrane antigen TM4 superfamily protein.

Human membrane antigen; TM4 superfamily protein; antibody; osteosarcoma; immunomodulation; diagnosis; cancer; chemotactic; haemotopoiesis; anti-inflammation; genetic fingerprinting; human CB63; antimicrobial; analgesic; fertility.

XX Homo sapiens.

XX WO9733993-AL.

PN 18-SEP-1997.

XX 14-MAR-1997; 97WO-JP000811.

XX 15-MAR-1996; 96JP-00059571.

XX (SAGA) SAGAMI CHEM RES CENTRE.

XX Kato S, Sekine S, Yamaguchi T;

XX WPI; 1997-470873/43.

XX N-PSDB; AAT84982.

XX Human membrane antigen of TM4 superfamily - useful to diagnose or treat


```
QY 1 ATGGGCCAGTGGCGCATCACCTCTCTCAAGACCGTGTGTTCTTCTCAACCTCATCTTC 60
DB 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAseLeuIlePhe 20
QY 61 TGGGGGCGAGCTGGCATTATATGCTATGTGGAGCCCTATGCTTTCATCATTATGATGAC 120
DB 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACCACTCTTTGAAGATGTGTACACGCTCATCTGCTGTAGTGATCATAGCTGTA 180
DB 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValIleIleAlaVal 60
QY 181 GGAGCCCTGCTTTTCATCTATGGGCTAATGGCTGTGTGCGCAATCCGGGAAGTCGC 240
DB 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysSalThrIleArgGluSerArg 80
QY 241 TGTGGACTTCCACGTTTGTTCATCATCTGCTCTTGGTTTGTTCACAGAAGTTGTGTA 300
DB 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
QY 301 GTGGTTTGGATATGTTTACAGAGCAAGGTGGAAATGAGTTGATCGCAGCATTCAG 360
DB 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAseGluValAspArgSerIleGln 120
QY 361 AAAGTGTATGAAGCACTCAATGAACCAACCTGATGCTGTAGCCGGGCTATTGATTAT 420
DB 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaLaserArgAlaIleAspTyr 140
QY 421 GTACAGAGACGTGCAATTTGTGGAAATTCACAATCTACAGACTGGGGAATAACAGAT 480
DB 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTyrTrpGluAseThrAsp 160
QY 481 TGTTCMAAGAAACCAAAACAGAGTGTCTCTTACGTCTGTAGCTGCTGCAGAGACTGCCAGC 540
DB 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATGGACCTGGCCGCCACCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
DB 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAAGCTACAAAGAAATCATGATGATGATCTGTGGCCGCCACTGGCATTGCA 660
DB 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
QY 661 GCTATTACGTCTGGGCGATGCTGTGTGCTGTGATCGTGTGTGTCAGAGAGCTAGAGAT 720
DB 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
QY 721 CCTGCTTACGAGCTCCTCATCATCTGGCGGAACCTATGCA 759
DB 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253
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RESULT 3

AAB92850
ID AAB92850 standard; protein; 253 AA.

XX AAB92850;
AC AAB92850;

XX
DT 26-JUN-2001 (first entry)
XX Human protein sequence SEQ ID NO:11412.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.

XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.

XX
PF 28-JUL-2000; 2000EP-00116126.

PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayaishi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

PS Claim 8; SEQ ID NO 11412; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

XX SQ Sequence 253 AA;

Alignment Scores:
Pred. No.: 1,32e-138 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 4 Gaps: 0

US-10-608-388A-1 (1-759) x AAB92850 (1-253)

QY 1 ATGGGGCAGTGGCGCATCACCTCTCAAGACCGTGTGTTCTTCTCAACCTCATCTTC 60
DB 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAseLeuIlePhe 20
QY 61 TGGGGGCGAGCTGGCATTATATGCTATGTGGAGCCCTATGCTTTCATCATTATGATGAC 120
DB 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACCACTCTTTGAAGATGTGTACACGCTCATCTGCTGTAGTGATCATAGCTGTA 180
DB 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValIleIleAlaVal 60
QY 181 GGAGCCCTGCTTTTCATCATCTGGGCTAATGGCTGTGTGCGCAATCCGGGAAGTCGC 240
DB 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysAlaThrIleArgGluSerArg 80
QY 241 TGTGGAATGGCCACGTTTGTTCATCATCTGCTGTGTTTGTTCACAGAAGTTGTGTA 300

81 CysGlyLeuAlaThrPheValIleLeuLeuLeuValPheValThrGluValValVal 100
301 GTGGTTTGGATATGTTTACAGACCAAGGTGAAAATGAGTTGATCCAGCATTCAG 360
101 ValValLeuGlyTyValTyArgAlaLysValGluAsnGluValAspArgSerIleGln 120
361 AAAGTGATTAAGACTCAATAGGAACCAACCTGATGCTGTACCGGGCTATTGATTAT 420
121 LysValTyLysThrTyAsnGlyThrAsnProAspAlaSerArgAlaIleAspTyr 140
421 GTACAGACAGCTGCATTTGTTGGAAATTCACAACTACTCAGACTGGGAAATACAGAT 480
141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTyrGluAsnThrAsp 160
481 TGGTTCAAGAAACCAAAACCAAGGTGCTCCCTCTTACGCTGCTCAGAGAGCTGCCAGC 540
161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysAspArgGluThrAlaSer 180
541 AATTGTAATGCGACCTGGCCACCCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
601 GTAGTGAAGAGCTACAGAATAATCATGATGATGATCTGTGGCCGCACTGGCATTTGCA 660
201 ValValLysLysLeuGlnGluIleMetMetHisValIleTyrAlaLeuAlaPheAla 220
661 GCTATTGAGCTGCTGGGATCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 240
721 CCTGCTTACGAGCTCTCATCACTGGCGGAACCTATGCA 759
241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

RESULT 4

AAB92830
ID AAB92830 standard; protein; 253 AA.

XX AAB92830;

XX 26-JUN-2001 (first entry)

XX Human protein sequence SEQ ID NO:11371.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX OS Homo sapiens.

XX EPI074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-00116126.

XX 29-JUL-1999; 99JP-00248036.

XX 27-AUG-1999; 99JP-00300253.

XX 11-JAN-2000; 2000JP-00118776.

XX 02-MAY-2000; 2000JP-00183767.

XX 09-JUN-2000; 2000JP-00241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX Claim 8; SEQ ID NO 11371; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

XX SQ Sequence 253 AA;

Alignment Scores:

Pred. No.: 1 32e-138 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.5% Indels: 0
DB: Gaps: 0

US-10-608-388A-1 (1-759) X AAB92830 (1-253)

Qy 1 ATGGGGCAGTGGCGCATCACCTCTCCAGACCGTGTGCTCTTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
Qy 61 TGGGGGCGAGCTGGCATTTTATGCTATGTGGAGCCTATGCTTCATCACCATTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
Qy 121 TATGACCACCTTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTGATCATAGCTGTA 180
Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValIleAlaVal 60
Qy 181 GGAGCCCTGCTTTTCATCATTTGGGCTAAATGGCTGTGCTGCCACAAATCCGGGAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
Qy 241 TGTGGACTTCCAGCTTTGTTCATCATCTCTGCTTTGTTTGTTCACAGAGTTGTTGTA 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuLeuValPheValThrGluValValVal 100
Qy 301 GTGGTTTGGGATATGTTTACAGACGCAAGGTGGAATGAGTTGATCGCAGCATTCAG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
Qy 361 AAGTGTTATAGACCTACAAATGGAAACCAACCTGATGCTGTAGCTAGCCGGCTATTGATTAT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
Qy 421 GTACAGAGACAGCTGCATTGTTGGAAATTCACAACTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTyrGluAsnThrAsp 160
Qy 481 TGGTTCAAGAAACCAAAACCAAGGTGCTCCCTCTTACGCTGCTCAGAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
Qy 541 AATTGTAATGCGACCTGGCCACCCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600

```
181 AsnCysaenGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
601 GTAGTGAAGAGCTACAGAAATCATGATCATGCTGCTGGCGCGCACTGGCATTTGCA 660
201 ValVallylsylLeuGlnGluMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
661 GCTATTACAGCTGCTGGCAGCTGCTGTGTCTTGGCATCTGTGTGTCAGAGAGTAGAGAT 720
221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgGlySerArgAsp 240
721 CTGCTTACGAGCTCTCATCTGCTGGCGGAGCACTATGCA 759
241 ProAlaTyrGluLeuLeuIleThrGlyThrTyrAla 253

RESULT 5
ABB84849
ID ABB84849 standard; protein; 253 AA.
XX
AC ABB84849;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO730 protein sequence SEQ ID NO:66.
XX
KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
PN WO20020690-A2.
XX
PD 03-JAN-2002.
XX
PF 20-JUN-2001; 2001WO-US019692.
XX
PR 23-JUN-2000; 2000US-0213637P.
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00646410.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 08-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
```

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25-MAY-2001; 2001WO-US017092.
30-MAY-2001; 2001US-00870574.
30-MAY-2001; 2001WO-US017443.
01-JUN-2001; 2001WO-US017800.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
XX
DR WPI; 2002-090516/12.
DR N-PSDB; ABL88104.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 66; 565pp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
XX
SQ Sequence 253 AA;

Alignment Scores:
Pred. No.: 1-32e-138 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 5 Gaps: 0

US-10-608-388A-1 (1-759) x ABB84849 (1-253)
QY 1 ATGGGCGCAGTCGGGCATCACCTCTCTCAAGACCGTCTGCTTTTCTCAACCTCATCTTC 60
DB 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAenLeuIlePhe 20
QY 61 TGGGGGGCAGCTGGGCATTTTATGCTATGTTGGAGCGCTATGCTTCTCATCTATGATGAC 120
DB 21 TrpGlyAlaAlaGlyIleLeuLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACCACTCTTTGAAGATGTACACGCTCATCCCTGCTGTAGTGTATCATGCTGTA 180
DB 41 TyrAspHisPhePheGluaspValTyrThrLeuIleProAlaValValIleAlaVal 60
QY 181 GGAGCCCTGCTTTTTCATCATTTGGGCTAAATTGGCTGTGTGCCCAATCCGGGAAGTCGC 240
DB 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
QY 241 TGTGGACTTGGCCAGCTTTGTGTGTCATCATCTCTGCTCTTGGTTTGTCTCAGAGAGTTGTA 300
DB 81 CysGlyLeuAlaThrPheValIleIleLeuLeuLeuValPheValThrGluValValVal 100
QY 301 GTGGTTTGGGATATGTTTACAGAGCAAGAGTGGAAATGAGTTTGTATCGCACATTTCAG 360
DB 101 ValValLeuGlyTyrValTyrArgAlaLysValGluasnGluValaspArgSerIleGln 120
QY 361 AAAGTGTATAGACCTCAATGGAACCAACCTGATGCTGTAGCGGGCTATTGATTAT 420
```

Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
 Qy 421 GTACAGACAGCTGCATTGTTGGAAATTCACAACTACTCAGACTGGGAAAATACAGAT 480
 Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
 Qy 481 TGGTTCAAGAAACCAAAACACAGAGTGTCCCTCTTAGCTGCTGCAGAGACTGCCAGC 540
 Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
 Qy 541 AATTGTAATGCAGCCTGGCCACCTTCGACCTCTATGCTAGGGGGTGTGAGGCTCTA 600
 Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
 Qy 601 GTAGTGAAGAGCTACAGAAATCATGATGATGATGCTGGCGCGCACTGGCATTTGCA 660
 Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
 Qy 661 GCTATTGAGCTGCTGGGATGCTGTGTGCTTGTGCATCGTGTGTGCAGAGGAGTAGAGAT 720
 Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
 Qy 721 CCTGCTTACAGACTCCTCATCATCTGGCGGAACCTATGCA 759
 Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253
 RESULT 6
 ABB95455
 ID ABB95455 standard; protein; 253 AA.
 AC ABB95455;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE Human angiogenesis related protein PRO730 SEQ ID NO: 66.
 KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiant; cytosclerotic; antiangiogenic; hypotensive; vulnerary;
 KW antiarteriosclerotic.
 OS Homo sapiens.
 XX
 PN WO200208284-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 09-JUL-2001; 2001WO-US021735.
 XX
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.

PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 XX
 PA (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERB/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J..
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI; 2002-171999/22.
 DR N-PSDB; ABL95593.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 PS Claim 11; Fig 66; 567pp; English.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a PRO protein of the invention
 XX
 SQ Sequence 253 AA;
 Alignment Scores:
 Pred. No.: 1.32e-138 Length: 253
 Score: 1336.00 Matches: 253
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 93.5% Indels: 0
 DB: 5 Gaps:
 US-10-608-388A-1 (1-759) x ABB95455 (1-253)
 Qy 1 ATGGCCAGTCGGCATCCTCTCCAGACCGTGTGTTCTTCTCAACCTCATCTTC 60
 Db 1 MetGlyGlnCysGlyIleThrSerSerIleThrValLeuValPheLeuAsnLeuIlePhe 20
 Qy 61 TGGGGGCGAGCTGGCATTATTTATGCTATGTGGAGCCCTATGTTCTTCATCACTTATGATGAC 120
 Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
 Qy 121 TATGACCACCTCTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTATCATGATCTGTA 180

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Db 41 TyraephHisPhePheGluAspValTyrThrLeuIleProAlaValValIleAlaVal 60
Qy 181 GGAGCCCTGTTTTCATCGGCTAATGGCTGCTGCCACATCCGGGAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
Qy 241 TGTGGACTTCCACAGTGTGTGCATCATCTCTTGTGTTTGTGCAGAGAAGTTGTGTA 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
Qy 301 GTGGTTTGGATATGTTTACAGACAAAGTGGAAATCAGGTTGATCCACAGATTGAG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
Qy 361 AAAGTGTATAGACCTACATCAATGAACCAACCTGATGCTGCTAGCCGGCTATTGATTAT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
Qy 421 GTACAGACAGCTGCATTTGTTGGAATTCACAACCTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
Qy 481 TGGTTCAAGAAACCAAAAACCGAGTGTCCCTCTTAGCTGTGCGAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
Qy 541 AATTGTAAAGCGACCTGGCCACCTTCCGACCTCTATGCTGAGGGGTGAGGCTCTTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
Qy 601 GTAGTGAAGAGCTACAAGAAATCATGATCATGTGATCTGGGCCGCACTGGCATTTGCA 660
Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
Qy 661 GCTATTGAGCTGTGGGCATGCTGTGTGTGTGCTGTGATGCTGTGTCAGAGAGGAGTAGAT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
Qy 721 CTGCTTACAGAGCTCTCATCTACCTGGCGGCACTTATGCA 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyTyrTyrAla 253

RESULT 7
ID AAE30341 standard; protein; 253 AA.
AC AAE30341;
XX
XX
XX 24-FEB-2003 (first entry)
XX Human tetraspan 3 protein.
XX
XX Brain; tumour protein target; Tbt; ischaemic stroke; cancer; epilepsy;
XX schizophrenia; depression; Alzheimer's disease; Parkinson's disease;
XX Huntington's chorea; traumatic head injury; dementia; stupor; headache;
XX coma; vertigo; weakness; myasthenia gravis; cerebrovascular disorder;
XX infection; multiple sclerosis; pregnancy; medical illness; vasotropic;
XX metabolic deficiency; cerebroprotective; antidepressant; antibacterial;
XX cytostatic; nootropic; analgesic; fungicide; virucide; tetraspan 3;
XX human.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 1..11
XX FT /note= "Cytoplasmic domain"
XX Domain 12..32
XX FT /note= "Transmembrane domain"
XX Domain 33..50
XX FT /note= "Extracellular domain"
XX Domain 51..71
XX FT /note= "Transmembrane domain"
XX Domain 72..85
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FT Domain /note= "Cytoplasmic domain"
FT 85..106
FT Domain /note= "Transmembrane domain"
FT 107..212
FT Domain /note= "Extracellular domain"
FT 213..233
FT Domain /note= "Transmembrane domain"
FT 234..235
FT Domain /note= "Cytoplasmic domain"
XX
XX W0200276510-A1.
XX
XX 03-OCT-2002.
XX
XX 22-MAR-2002; 2002WO-US008992.
XX
XX 23-MAR-2001; 2001US-00816703.
PR 17-OCT-2001; 2001US-00983000.
XX
XX (AGYT-) AGY THERAPEUTICS INC.
XX
XX Mueller S, Melcher T, Chin DJ;
XX
XX WPI; 2003-029903/02.
DR N-PSDB; AAD48134.
XX
XX Developing active agents that modulate the activity of a brain tumor
XX protein target gene or gene product for treating e.g. stroke or cancer,
XX comprises contacting an agent with a brain tumor protein.
XX
XX Claim 1; Page 125-127; 135pp; English.
XX
XX The invention relates to a method for developing biologically active
XX agents that modulate activity of a brain tumour protein target (Tbt) gene
XX or gene product. The method is useful for developing biologically active
XX agents that modulate the activity of a brain tumour protein target gene
XX or gene product. Compounds that bind to the brain tumour proteins are
XX useful for treating e.g. ischaemic stroke, brain cancer, epilepsy,
XX schizophrenia, depression, Alzheimer's disease, Parkinson's disease,
XX Huntington's chorea, traumatic head injury, dementia, stupor, headache,
XX coma, vertigo, weakness, myasthenia gravis, cerebrovascular disorders,
XX infectious disorders (including fungal, bacterial, viral and parasitic
XX infections), multiple sclerosis, and other complications associated with
XX pregnancy, medical illness, alcohol and substance abuse, toxins and
XX metabolic deficiencies. The brain tumour proteins may also be used to
XX raise antibodies. The present sequence is human tetraspan 3 protein used
XX to illustrate the method of the invention
XX
XX Sequence 253 AA;
```

```
Alignment Scores:
Pred. No.: 1.32e-138 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 6 Gaps: 0
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US-10-608-388A-1 (1-759) x AAE30341 (1-253)

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Qy 1 ATGGGCCAGTGGCGCATCACCTCTCCAGAGCCGTGGTCTTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
Qy 61 TGGGGGGCAGCTGGCATTATGCTTATGTGGGAGCCTATGCTTTCATCATCTTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
Qy 121 TATGACCACTTCTTTGAAGATGTGTACAGCTCATCCCTGCTGTAGTGTAGTGTGTA 180
Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleAlaVal 60
Qy 181 GGAGCCCTGCTTTTTCATCATTTGGGGCTAATTGGCTGCTGTGCCACAATCCGGGAAGTCGC 240
```

Db 61 GlyAlaLeuLeuPheLeuLeuGlyCysCysAlaThrLeuArgGluSerArg 80
 Qy 241 TGTGGACTTGCACGTTTGTGCATCATCTGCTGTTTGTTCACAGAGTTGTGTA 300
 Db 81 CysGlyLeuAlaThrPheValLeuLeuLeuValPheValThrGluValValVal 100
 Qy 301 GTGGTTTGGATATGTTACAGACCAAGGTGGAATGAGTTGATCCGACGATTCAG 360
 Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
 Qy 361 AAAGTGATTAAGACTCAATAGGAACCAACCTGCTAGCTAGCCGGCTATTGATTAT 420
 Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaLysArgAlaIleAspTyr 140
 Qy 421 GTACAGACAGACTGCATTGTTGGAAATTCACAACTACTCAGACTGGGAAATACAGAT 480
 Db 141 ValGlnArgGlnLeuHisCysCysGlyLeuHisAsnTyrSerAspTyrGluAsnThrAsp 160
 Qy 481 TGGTTCAAGAAACCAAAACCAAGAGTGTCCCTCTTACCTGCTGCAGAGACTGCCAGC 540
 Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
 Qy 541 AATGTGTAATGCGACCTGGCCACCCTTCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
 Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
 Qy 601 GTAGTGAAGAGCTACAGAAATCATGATGATGATGATCTGGGCGCCACTGGCATTTGCA 660
 Db 201 ValValLysLysLeuGlnGluLeuMetMetHisValIleTyrAlaLeuAlaPheAla 220
 Qy 661 GCTATTGAGCTGGGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 240
 Qy 721 CCTGCTTACGAGCTCCTCATCACTGGCGGAACCTATGCA 759
 Db 241 ProAlaTyrGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 253

RESULT 8

ADD14059
 ID ADD14059 standard; protein; 253 AA.
 AC ADD14059;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human src biomarker polypeptide SEQ ID NO:248.
 XX
 KW predictor set; protein tyrosine kinase activity modulator;
 KW protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
 KW gene therapy; drug sensitivity; genetic profile; cancer; human.
 XX
 OS Homo. sapiens.
 XX
 PN WO2003062395-A2.
 XX
 PD 31-JUL-2003.
 XX
 PF 17-JAN-2003; 2003WO-US0001981.
 XX
 PR 18-JAN-2002; 2002US-0350061P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Huang F, Fairchild CR, Lee FY, Shaw P;
 XX
 DR WPI; 2003-636735/60.
 DR N-PSDB; ADD14654.
 XX
 PT New polynucleotides and polypeptides for predicting the activity of
 PT compounds that interact with protein tyrosine kinases and/or protein
 PT tyrosine kinase pathways.

XX
 PS
 XX Claim 10; SEQ ID NO 248; 139pp; English.
 CC The present invention describes a predictor set comprising a plurality of
 CC polynucleotides or polypeptides whose expression pattern is predictive of
 CC the response of cells to treatment with a compound that modulates protein
 CC tyrosine kinase activity or members of the protein tyrosine kinase
 CC pathway. Also described: (1) predicting whether a compound is capable of
 CC modulating the activity of cells, comprising obtaining a sample of cells,
 CC determining whether the cells express a plurality of markers, and
 CC correlating the expression of the markers to the compound's ability to
 CC modulate the activity of the cells; (2) a plurality of cell lines for
 CC identifying polynucleotides and polypeptides whose expression levels
 CC correlate with compound sensitivity or resistance of cells associated
 CC with a disease state; and (3) identifying polynucleotides and
 CC polypeptides that predict compound sensitivity or resistance of cells
 CC associated with a disease state, comprising subjecting the plurality of
 CC cell lines to one or more compounds, analysing the expression pattern of
 CC a microarray of polynucleotides or polypeptides, and selecting
 CC polynucleotides or polypeptides that predict the sensitivity or
 CC resistance of cells associated with a disease state by using the
 CC expression pattern of the microarray. The polynucleotides and
 CC polypeptides have cytostatic activities, and can be used in gene therapy.
 CC The polynucleotides and polypeptides are useful in predicting the
 CC activity of compounds that interact with protein tyrosine kinases and/or
 CC protein tyrosine kinase pathways. These may be used in determining drug
 CC sensitivity in patients to allow the development of individualized
 CC generic profiles which aid in treating diseases and disorders (e.g.
 CC cancer) based on patient response at a molecular level. The present
 CC sequence is used in the exemplification of the present invention.

XX
 SQ Sequence 253 AA;

Alignment Scores:

Pred. No.: 1,32e-138 Length: 253
 Score: 1336.00 Matches: 253
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 93.5% Indels: 0
 DB: Gaps: 0

US-10-608-388A-1 (1-759) x ADD14059 (1-253)

Qy 1 ATGGGCGCAGTGGCGCATCACTCTCCAGACGCTGCTGCTTCTTCAACCTCATCTTC 60
 Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
 Qy 61 TGGGGGCGAGCTGGCATTTTATGCTATGTGGAGCCTATGCTTTCATCATCTATGATGAC 120
 Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
 Qy 121 TATGACCACTTCTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTGATCATAGCTGTA 180
 Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValIleIleAlaVal 60
 Qy 181 GGAGCCCTGCTTTTTCATTCATTTGGCTAATTTGGCTGTGTCGCCAATCCGGGAAAGTCG 240
 Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
 Qy 241 TGTGGACTTGCACGTTTGTGCATCATCTGCTGTTTGTGTTTGTGTCAGAGTTGTGTA 300
 Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuLeuValPheValThrGluValValVal 100
 Qy 301 GTGGTTTGGATATGTTTACAGACCAAGGTGGAATGAGTTGATCCGACGATTCAG 360
 Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
 Qy 361 AAAGTGATTAAGACTCAATAGGAACCAACCTGCTAGCTAGCCGGCTATTGATTAT 420
 Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaLysArgAlaIleAspTyr 140
 Qy 421 GTACAGACAGCTGCATTGTTGGAAATTCACAACTACTCAGACTGGGAAATACAGAT 480

Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrsrAspTrpGluAsnThrAsp 160
Qy 481 TGGTTCAAAGAAACCAAAACACAGAGTGTCTCTTAGCTGTGACAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
Qy 541 AATTGTAAATGACAGCTGGCCACCTTCCGACTCTATGCTGAGGGGTGTGAGGCTCTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyraGluGlyCysGluAlaLeu 200
Qy 601 GTACTGAAGAGCTACAGAAATCATGATCATGCTGCTGGCGGCACTGGCAATTGCA 660
Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
Qy 661 GCTATTGACGTGCTGGGCATGCTGTGCTTGCATCGTGTGTGACAGAGAGTAGAGAT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
Qy 721 CTGTCTTACGAGCTCTCATCATCTGCGGGAACCTATGCA 759
Db 241 ProAlaTyraGluLeuLeuIleThrGlyGlyThrTyraAla 253

RESULT 9

ADD10355
ID ADD10355 standard; protein; 253 AA.

XX AC ADD10355;

XX DT 01-JAN-2004 (first entry)

XX DE Human secreted/transmembrane PRO polypeptide #33.

XX KW human; secreted protein; transmembrane protein; cardiovascular disorder;
KW endothelial disorder; angiogenic disorder; myocardial infarction;
KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.

XX OS Homo sapiens.

XX PN US2003105011-A1.

XX PD 05-JUN-2003.

XX PF 16-AUG-2002; 2002US-00223084.

XX PR 15-SEP-2000; 2000US-0232887P.

XX PR 20-JUN-2001; 2001WO-US019692.

XX PR 09-JUL-2001; 2001WO-US021735.

XX PR 20-FEB-2002; 2002US-00081056.

XX PA (GETH) GENENTECH INC.

XX PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

XX PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;

XX PI Watanabe CK, Williams PM, Wood WI, Ye W;

XX XX WPI; 2003-810831/76.

XX DR N-PSDB; ADD10354.

XX XX New isolated nucleic acid encoding a secreted and transmembrane

PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
PT disorder in a mammal, such as cancer or age-related macular degeneration.
XX Claim 11; SEQ ID NO 66; 493pp; English.
XX The invention relates to an isolated nucleic acid encoding a secreted and
CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterised by the presence of

CC an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis. A PRO
CC PRO4302, or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to
CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents the amino acid
CC sequence of a PRO polypeptide of the invention.

XX SQ Sequence 253 AA;

Alignment Scores:
Pred. No.: 1-32e-138 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 7 Gaps: 0

US-10-608-388A-1 (1-759) x ADD10355 (1-253)

Qy 1 ATGGGGCAGTGGGGCATCATCTCTCCAGACCGTGTGTCTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
Qy 61 TGGGGGGCAGTGGGCATTTTATGCTATGTGGGAGCTATGCTTCTCATCTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyIleLeuCysTyraGlyAlaTyraValPheIleThrTyraAsp 40
Qy 121 TATGACCACCTCTTTGAAGATGTGTACAGCTCATCTCTGCTGTAGTGATCATAGCTGTA 180
Db 41 TyrAspHisPhePheGluAspValTyraThrLeuLeuProAlaValValIleAlaVal 60
Qy 181 GGAGCCCTGCTTTTCATCTTGGCTTAATGGCTGTGTGCCACATCCGGGAAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
Qy 241 TGTGGACTTGGCCACGTTTGTTCATCTCTGCTCTCTGTTTTCACAGAGTGTGTGTA 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuLeuValPheValThrGluAlaVal 100
Qy 301 GTGGTTTGGGATATGTTTACAGAGCAAAAGTGGAAATCAGCTTGTATCGCAGCATTCAG 360
Db 101 ValValLeuGlyTyraValTyraGlyAlaLysValGluAsnGluValAspArgSerIleGln 120
Qy 361 AAGTGTATAAGACCTACAAATGGAAACCAACCTGTATGCTGTAGCGGGCTATTGATTAT 420
Db 121 LysValTyraLysThrTyraAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
Qy 421 GTACAGAGACAGCTGCTTGTGTGAATTCACACTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrsrAspTrpGluAsnThrAsp 160
Qy 481 TGGTTCAAAGAAACCAAAACACAGAGTGTCTCTTGTAGCTGTGACAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
Qy 541 AATTGTAAATGACAGCTGGCCACCTTCCGACTCTATGCTGAGGGGTGTGAGGCTCTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyraGluGlyCysGluAlaLeu 200
Qy 601 GTAGTGAGAGACACAGAAATCATGATGATGATCTGGGCCCGCAGCTGGCATTTGCA 660
Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
Qy 661 GCTATTGACGTGCTGGGCATGCTGTGTGTGCTGTGCATCGTGTGTGACAGAGAGTAGAGAT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
Qy 721 CTGTCTTACGAGCTCTCATCATCTGCGGGAACCTATGCA 759
Db 241 ProAlaTyraGluLeuLeuIleThrGlyGlyThrTyraAla 253

PD 05-JUN-2003.
 XX PF 16-AUG-2002; 2002US-00223088.
 XX PR 15-SEP-2000; 2000US-0322887P.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 20-FEB-2002; 2002US-00081056.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Ferrara N, Gerber H, Gerritsen MB, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
 PI Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI: 2003-829354/77.
 DR N-PSDB; ADD37107.
 XX
 PT New isolated nucleic acids encoding a secreted and transmembrane
 PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
 PT disorder in a mammal, such as cancer or age-related macular degeneration.
 XX
 PS Claim 11; SEQ ID NO 66; 492pp; English.
 XX
 CC The invention relates to an isolated nucleic acid encoding a secreted and
 CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
 CC by the nucleic acid, or an agonist or antagonist, is used to treat a
 CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
 CC preferably a human. The human may have suffered a myocardial infarction
 CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
 CC degeneration. The cardiac hypertrophy is characterized by the presence of
 CC an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
 CC specification, or an agonist is used to inhibit or stimulate endothelial
 CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
 CC hypertrophy. PRO137 or an agonist is used to stimulate angiogenesis.
 CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
 CC polypeptide, given in the specification, or an agonist is used to
 CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
 CC cell tube formation. The present sequence represents the amino acid
 CC sequence of a PRO polypeptide of the invention.
 XX
 SQ Sequence 253 AA;
 Alignment Scores:
 Pred. No.: 1 32e-138 Length: 253
 Score: 1336.00 Matches: 253
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 93.5% Indels: 0
 DB: 7 Gaps: 0
 US-10-608-388A-1 (1-759) x ADD37108 (1-253)
 QY 1 ATGGGGCAGTGGCGCATCCTCTCCAGACCGTGTCTTCTCAACCTCATCTTC 60
 Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
 QY 61 TGGGGGCGAGCTGGCATTTTATGCTATGTGGAGCGCTATGCTTCTCATCTATGATGAC 120
 Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
 QY 121 TATGACCATCTCTTCAAGATGTCACGCTCATCCCTGCTGTAGTCATGATGTA 180
 Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValIleIleAlaVal 60
 QY 181 GGAGCCCTGCTTTTTCATCTATGGGCTAATGGCTGTGTGCCACAATCCGGAAAGTCG 240
 Db 61 GlyAlaLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
 QY 241 TGTGACCTTGCACGTTTGTATCATCTCTGCTCTTGTGTTTGTACAGAGTTGTGTA 300
 Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuLeuValPheValThrGluValValVal 100

QY 301 GTGGTTTGGGATATGTTTACAGAGCAAAAGGTGGAATAGAGTTGATCCAGCATTCAG 360
 Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
 QY 361 AAAGTGTATAGACTTACATCAATGGAACCAACCTGTAGTGTCTAGCGGGCTATTGATTAT 420
 Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
 QY 421 GTACGAGACAGCTGCATTGTTGTGAATTCAACTACTCTACAGCTGGGAATAACAGAT 480
 Db 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
 QY 481 TGGTTCAAAAGAAACCAAAACCAGAGTGTCCCTCTTGTAGTGTCTGACAGAGACTGCCAGC 540
 Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
 QY 541 AATTGTATGGCAGCTGCGCCACCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTTA 600
 Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
 QY 601 GTAGTGAAGAAGCTACAAGAAATCATGATGTCATGTCATCTGGSCCGCAGCTGGCATTTGCA 660
 Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
 QY 661 GCTATTACAGTCTGCGCATGCTGTGTGCTTGCATGCTTGTGTCAGAGGAGTAGAGAT 720
 Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
 QY 721 CTGCTTACGAGCTCTCTCATCATCTGCGGGAACCTATGCA 759
 Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253
 RESULT 12
 ADD45736
 ID ADD45736 standard; protein; 253 AA.
 XX
 AC ADD45736;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein O60637, SEQ ID NO 11404.
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX Homo sapiens.
 OS
 XX WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; O60637.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,

CC polypeptide, given in the specification, or an agonist is used to stimulate or inhibit smooth muscle cell growth, or to induce endothelial cell tube formation. The present sequence represents the amino acid sequence of a PRO polypeptide of the invention.

XX SQ Sequence 253 AA;

Alignment Scores:

Pred. No.: 1.32e-138 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 8 Gaps: 0

US-10-608-388A-1 (1-759) x ADE41316 (1-253)

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QY 1 ATGGGCGAGTGGCGATCACCCTCTCAAGACCTGCTGCTTTCTCAACCTCATCTTC 60
DB 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
QY 61 TGGGGGCGAGTGGCGATTTATGCTATGTGGAGCCTATGCTTCATCATCTATGATGAC 120
DB 21 TrpGlyAlaAlaGlyIleLeuCysGlyTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACCACTCTTTGAAGATGTGTACACGCTCATCCTGCTGTAGTGATCATAGCTGTA 180
DB 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleAlaVal 60
QY 181 GAGCCCTGCTTTTCATCATTTGGGCTAATGGCTGTGCTGTGCGCAATCGGGAAAGTCG 240
DB 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
QY 241 TGTGGAGTCCGAGTTGTTCATCATCTGCTCTGCTGCTTTGTCACAGAGTTGTGTA 300
DB 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
QY 301 GTGGTTTGGGATATGTTTACAGAGCAAGGTGAAATGAGTTGATCGCAGCATTCAG 360
DB 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
QY 361 AAAGTGTATAGACCTACAATGGAAACCAACCTGATGCTGCTAGCCGGCTATTGATTAT 420
DB 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGACAGCTGCATTTGTTGGATTCACAACTACTCAGACTGGGAAATACAGAT 480
DB 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
QY 481 TGGTTCAAGAAACCAAAACCAAGAGTGCTCCTTGTAGCTGTCACAGAGACTGCCAGC 540
DB 161 TrpPheLysGlnThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATGGACCTGGCCCACTTCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
DB 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAGCTACAGAAATCATGATGATGATGCTGGGCGGCGACTGGCATTTGCA 660
DB 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
QY 661 GCTATTACAGCTGCTGGGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
QY 721 CTGCTTTACAGCTCTCTCATCTGCGGGAACCTATGCA 759
DB 241 ProAlaTyrGluLeuLeuIleThrGlyThrTyrAla 253
```

RESULT 14

ADH43499

ID ADH43499 standard; protein; 253 AA.

XX

AC ADH43499;

XX 25-MAR-2004 (first entry)

XX Human PRO polypeptide #33.

DE Human; PRO; cardiovascular disorder; endothelial disorder;
XX angiogenic disorder; endothelial cell growth; cardiac hypertrophy;
XX cell apoptosis; cell tube formation; angiogenesis;
XX smooth muscle cell growth; myocardial infarction; trauma; cancer;
XX age-related macular degeneration; cytostatic; cardiant;
XX cerebroprotective; ophthalmological; vulnery.

OS Homo sapiens.

XX US2003224984-A1.

XX 04-DEC-2003.

XX 26-NOV-2002; 2002US-00305654.

XX 20-JUN-2001; 2001WO-US019692.

XX (GETH) GENENTECH INC.

XX Baker KP, Ferrara N, Gerber H, Gertitsen ME, Goddard A,
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
XX WPI; 2004-042166/04.

DR N-PSDB; ADH43498.

XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
PT for treating myocardial infarction, cardiac hypertrophy, trauma, cancer,
PT or age-related macular degeneration.

XX Claim 11; SEQ ID NO 66; 492pp; English.

XX The invention relates to human PRO polypeptides and the PRO
CC polynucleotides encoding them. The invention also relates to treating
CC cardiovascular, endothelial or angiogenic disorders in mammals,
CC inhibiting endothelial cell growth, stimulating endothelial cell growth,
CC inducing cardiac hypertrophy, cell apoptosis or cell tube formation and
CC stimulating angiogenesis or smooth muscle cell growth by administering
CC polypeptides of the invention. The PRO polypeptides and polynucleotides
CC are useful for treating cardiovascular, endothelial or angiogenic
CC disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma,
CC cancer or age-related macular degeneration. The PRO polynucleotides are
CC useful as hybridisation probes in chromosome and gene mapping and in
CC generating antisense RNA and DNA, and for chromosome identification and
CC tissue typing. The PRO polypeptides and polynucleotides are also useful
CC in gene therapy and as molecular weight markers for protein
CC electrophoresis purposes. This sequence represents a human PRO
XX polypeptide of the invention.

XX Sequence 253 AA;

Alignment Scores:

Pred. No.: 1.32e-138 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 8 Gaps: 0

US-10-608-388A-1 (1-759) x ADH43499 (1-253)

QY 1 ATGGGCGAGTGGCGATCACCCTCTCAAGACCTGCTGCTTTCTCAACCTCATCTTC 60

DB 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20

QY 61 TGGGGGCGAGTGGCGATTTATGCTATGTGGAGCCTATGCTTCATCATCTATGATGAC 120

```
Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
Qy 121 TATGACCACTTCTTTGAAGATGTGTACAGGCTATCCCTGCTGTAGTCATCATAGCTGTA 180
Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleAlaVal 60
Qy 181 GGAGCCCTGCTTTTCATCATTTGGGCTAATTGGCTGCTGTGCACAAATCGGGAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysAlaThrIleArgGluSerArg 80
Qy 241 TGTGGACTTGGCACGTTTGTTCATCATCTGCTCTCTGTTTGTTCACAGAAAGTTGTGTA 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
Qy 301 GTGGTTTGGGATATGTTTACAGACCAAGCTGGGAATGAGTTGATCGCAGCATTCAG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
Qy 361 AAAGTGATAAGACCTACAATGGGAACCAACCTGATGCTGTAGCCGGCTATTGATTAT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaIleSerArgAlaIleAspTyr 140
Qy 421 GTACAGACAGCTGCTATTGTTGGAATTCACAACTACTCAGACTGGGAAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
Qy 481 TGGTTCAAAGAAACCAAAAACAGAGTGTCCCTCTTAGCTGCTGTGCAGAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
Qy 541 AATTGTATGTCAGCTGGCCCAACCTTCCGACCTCTATGCTGAGGGGTGAGGCTCTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
Qy 601 GTAGTGAAGAAGCTACAGAATAATCATGATGTGATCTGTGGCGGCACTGGCAATTTGCA 660
Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
Qy 661 GCTATTACGCTGTGGGATGCTGTGTGCTGTCATCGTGTGTCAGAGAGAGTAGAGAT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 240
Qy 721 CCTGCTTACGAGCTCTCTCATCTGCGGCAACCTATGCA 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyThrTyrAla 253
RESULT 15
ADJ75383
ID ADJ75383 standard; protein; 253 AA.
XX AC ADJ75383;
XX XX
XX 20-MAY-2004 (first entry)
XX DE Marker gene related amino acid sequence SEQ ID NO:635.
XX KW bronchial asthma; chronic obstructive pulmonary disease;
XX KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
XX KW gene therapy; marker.
XX OS Homo sapiens.
XX XX
XX FN EP1394274-A2.
XX XX
XX PD 03-MAR-2004.
XX XX
XX PF 04-AUG-2003; 2003EP-00254857.
XX XX
XX PR 06-AUG-2002; 2002JP-00229312.
XX PR 20-MAR-2003; 2003JP-00077212.
XX XX
XX PA (GENO-) GENOX RES INC.
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PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
XX WPI; 2004-193155/19.
XX
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample
PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.
XX
XX Example 11; SEQ ID NO 635; 241pp; English.
XX
XX The present invention describes a method of testing for bronchial asthma
XX or chronic obstructive pulmonary disease. The method comprises
CC determining the expression level of a marker gene in a biological sample
CC from a subject, comparing the expression level determined with the
CC expression level of the marker gene in a biological sample from a healthy
CC subject, and judging whether the subject has bronchial asthma or chronic
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC genes (S1) whose expression levels increase when respiratory epithelial
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC whose expression levels decrease when respiratory epithelial cells are
CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
CC testing for bronchial asthma or chronic obstructive pulmonary disease;
CC (2) a kit for screening for a candidate compound for a therapeutic agent
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC an animal model for bronchial asthma or chronic obstructive pulmonary
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC method for producing an animal model for bronchial asthma or chronic
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
CC asthma or chronic obstructive pulmonary disease, comprising the compound,
CC a marker gene or an antisense nucleic acid corresponding to a portion of
CC the marker gene, a ribozyme, a polynucleotide that suppresses the
CC expression of the gene through an RNAi effect or an antibody recognising
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
CC probe has been immobilised to assay a marker gene. (I) has respiratory
CC and antiasthmatic activities, and can be used in gene therapy. The method
CC is useful for testing for or screening for a therapeutic agent for
CC bronchial asthma or chronic obstructive pulmonary disease. The present
CC sequence is used in the exemplification of the present invention.
XX
XX Sequence 253 AA;
```

```
Alignment Scores:
Pred. No.: 1-32e-138 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 8 Gaps: 0
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US-10-608-388A-1 (1-759) x ADJ75383 (1-253)

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Qy 1 ATGGGCGAGTCGCGCATCACCTCTCCAGACCGTGTGCTTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
Qy 61 TGGGGGCGAGCTGGCATTTTATGCTATGTGGAGCCCTATGCTTCATCATTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
Qy 121 TATGACCACTTCTTTGAAGATGTGTACAGCTCATCTGCTGTAGTCATCATAGCTGTA 180
Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleAlaVal 60
Qy 181 GGAGCCCTGCTTTTCATCATTTGGGCTAATTGGCTGCTGTGCACAAATCGGGAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysAlaThrIleArgGluSerArg 80
Qy 241 TGTGGACTTGGCACGTTTGTTCATCATCTGCTCTCTGTTTGTTCACAGAAAGTTGTGTA 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
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QY 301 GTGGTTTGGGATATGTTTACAGAGCAAGGTGGAATAAGAGTTGATCGCAGCATTTGAG 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
QY 361 AAAGTGATAAGACCTACAAATGGAACCAACCCCTGATGCTGCTAGCCGGGCTATTGATTAT 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
QY 481 TGGTTCAAGAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATGGCAGCTGGCCCAACCTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTCAAGAGCTACAGAAATCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
QY 661 GCTATTTCAGCTGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 240
QY 721 CCTGCTTACGAGCTCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 759
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

Search completed: April 4, 2006, 21:24:08
Job time : 170 secs

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 4, 2006, 21:18:44 ; Search time 44.6 Seconds
(without alignments)
2401.327 Million cell updates/sec

Title: US-10-608-388a-1

Perfect score: 1429

Sequence: 1 atggggcagcgccgcatcac.....tactggcggaacctatgca 759

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=framet_n2p.model -DEV=xlip
-Q=/abss/ABSSWEB_spool/US10608388/runat_04042006_150648_14038/app_query.fasta_1
-DB=Uniprot -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pf0 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10608388 @CGN_1_1466 @runat_04042006_150648_14038 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMBOUT=120
-WARN TIMBOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------------|---------------------|
| 1 | 1336 | 93.5 | 253 | 1 TSN3 HUMAN | O60637 homo sapien |
| 2 | 1336 | 93.5 | 253 | 2 Q5RE11_PONPY | O5re11 pongo pygma |
| 3 | 1301 | 91.0 | 253 | 1 TSN3 MOUSE | O9qv33 mus musculus |
| 4 | 1301 | 91.0 | 253 | 2 Q54511_MOUSE | O54511 mus musculus |
| 5 | 1297 | 90.8 | 253 | 2 Q66H06_RAT | O66H06 rattus norv |
| 6 | 1293 | 90.5 | 253 | 2 Q80XR4_MOUSE | Q80xr4 mus musculus |
| 7 | 1186 | 83.0 | 253 | 2 Q4V915_BRARE | Q4v915 brachydanio |
| 8 | 1165 | 81.5 | 253 | 2 Q4FZN3_XENLA | Q4fnz3 xenopus lae |
| 9 | 1147 | 80.3 | 253 | 2 Q5XH66_XENLA | O5xh66 xenopus lae |
| 10 | 1140 | 79.8 | 253 | 2 Q4SAH7_TETNG | Q4sah7 tetraodon n |
| 11 | 1133 | 79.3 | 245 | 2 Q8BP22_MOUSE | Q8bp22 mus musculus |
| 12 | 1089 | 74.8 | 251 | 2 Q4SRU43_TETNG | Q4sr43 tetraodon n |
| 13 | 607 | 42.5 | 271 | 2 Q4RLU59_TETNG | Q4rl59 tetraodon n |
| 14 | 599 | 41.9 | 243 | 2 Q6NMG0_BRARE | Q6nwg0 brachydanio |
| 15 | 527.5 | 36.9 | 240 | 2 Q6GP11_XENLA | Q6gp11 xenopus lae |
| 16 | 522.5 | 36.6 | 240 | 2 Q6P7J5_XENLA | Q6p7j5 xenopus lae |

| | | | | | | |
|----|-------|------|-----|---|--------------|---------------------|
| 17 | 430.5 | 30.1 | 245 | 2 | Q5PQ10_XENLA | O5pq10 xenopus lae |
| 18 | 370 | 25.9 | 252 | 2 | Q5XJD1_BRARE | O5xjd1 brachydanio |
| 19 | 367 | 25.7 | 256 | 2 | Q4RS66_TETNG | Q4rs66 tetraodon n |
| 20 | 358.5 | 25.1 | 252 | 2 | Q5Z1I8_CHICK | O5z1i8 gallus gall |
| 21 | 358 | 25.1 | 237 | 2 | Q6P2T9_BRARE | O6p2t9 brachydanio |
| 22 | 344 | 24.1 | 253 | 1 | CD151_MOUSE | O35566 mus musculus |
| 23 | 343.5 | 24.0 | 244 | 1 | TSN7_PANTR | O7yq10 pan troglod |
| 24 | 343.5 | 24.0 | 244 | 2 | Q723Z6_HUMAN | O723z6 homo sapien |
| 25 | 343.5 | 24.0 | 249 | 1 | TSN7_HUMAN | P41732 h tetraspan |
| 26 | 342 | 23.9 | 253 | 1 | CD151_RAT | Q9qza6 rattus norv |
| 27 | 338.5 | 23.7 | 254 | 2 | Q6P031_BRARE | O6p031 brachydanio |
| 28 | 338 | 23.7 | 253 | 2 | Q921J7_MOUSE | O921j7 mus musculus |
| 29 | 337 | 23.6 | 253 | 2 | Q6DD13_XENLA | O6dd13 xenopus lae |
| 30 | 336 | 23.5 | 236 | 1 | CD63_BOVIN | O9xsk2 bos taurus |
| 31 | 335.5 | 23.5 | 249 | 2 | Q4RS43_MACFA | O4rs43 macaca fasc |
| 32 | 335 | 23.4 | 253 | 1 | CD151_CERAE | P61170 cercopithec |
| 33 | 335 | 23.4 | 253 | 1 | CD151_MACMU | P61171 macaca mula |
| 34 | 334.5 | 23.4 | 244 | 2 | Q6PDN6_MOUSE | O6pdn6 mus musculus |
| 35 | 334.5 | 23.4 | 249 | 1 | TSN7_MOUSE | O62283 mus musculus |
| 36 | 333.5 | 23.3 | 245 | 1 | TSN6_HUMAN | O43657 homo sapien |
| 37 | 333.5 | 23.3 | 245 | 1 | TSN6_MOUSE | O70401 mus musculus |
| 38 | 333.5 | 23.3 | 245 | 2 | Q6TAN9_HUMAN | O6tan9 homo sapien |
| 39 | 333.5 | 23.3 | 245 | 2 | Q54A42_HUMAN | O54a42 homo sapien |
| 40 | 333.5 | 23.3 | 245 | 2 | Q99L96_MOUSE | O99l96 mus musculus |
| 41 | 333.5 | 23.3 | 285 | 2 | Q59ED5_HUMAN | O59ed5 homo sapien |
| 42 | 332.5 | 23.3 | 244 | 1 | TSN7_PONPY | O7yqk9 pongo pygma |
| 43 | 332.5 | 23.3 | 245 | 2 | Q5RA55_PONPY | Q5ra55 pongo pygma |
| 44 | 332.5 | 23.3 | 246 | 2 | Q5R515_PONPY | O5r515 pongo pygma |
| 45 | 332 | 23.2 | 253 | 2 | Q53FU5_HUMAN | O53fu5 homo sapien |

ALIGNMENTS

RESULT 1
TSN3_HUMAN
ID TSN3 HUMAN STANDARD; PRT; 253 AA.
AC O60637; Q9BW22; Q9NVX9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tetraspanin-3 (Tspan-3) (Transmembrane 4 superfamily member 8)
DE (Tetraspanin TM4-A).
GN Name=TSN3; Synonyms=TM4SP8;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=98390278; PubMed=9714763; DOI=10.1016/S0167-4781(98)00087-6;
RA Todd S.C., Doctor V.S., Levy S.;
RT "Sequences and expression of six new members of the tetraspanin/TM4SF family";
RL Biochim. Biophys. Acta 1399:101-104(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Puls K.L., Ni J., Liu D., Morahan G., Wright M.D.;
RT "The molecular characterization of four tetraspanins";
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahori K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi K., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoaka S., Chiba Y.,

RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Mueashino K., Yuuki H., Oshima A., Sasaki N., Aoteuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiya M., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiya M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki H., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Oktani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs";
RL Nat. Genet. 36:40-45(2004).

[4]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Cervix, Colon, Muscle, and Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shellen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Regulates the proliferation and migration of
CC oligodendrocytes, a process essential for normal myelination and
CC repair (By similarity).
CC -!- SUBUNIT: Interacts with claudin 11 and integrins (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR EMBL; AF054840; AAC69716.1; -; mRNA.
DR EMBL; AF133423; AAF08362.1; -; mRNA.
DR EMBL; AK001326; BAA91627.1; -; mRNA.
DR EMBL; AK001305; BAA91613.1; -; mRNA.
DR EMBL; AK001310; BAA91615.1; -; mRNA.
DR EMBL; BC000704; AAH00704.1; -; mRNA.
DR EMBL; BC004280; AAH04280.1; -; mRNA.
DR EMBL; BC009248; AAH09248.1; -; mRNA.
DR EMBL; BC011206; AAH11206.1; -; mRNA.
DR PIR; A59264; A59264.
DR Ensembl; ENSG00000140391; Homo sapiens.
DR HGNC; HGNC:17752; TSPAN3.
DR H-InvDB; HIX0012461; -.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR000301; Transmem_4.

PFam: PF00335; Tetraspannin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
KW Glycoprotein; Transmembrane.
FT TOPO_DOM 1 11 Cytoplasmic (Potential).
FT TRANSMEM 12 32 Potential.
FT TOPO_DOM 33 50 Extracellular (Potential).
FT TRANSMEM 51 71 Extracellular (Potential).
FT TOPO_DOM 72 85 Cytoplasmic (Potential).
FT TRANSMEM 86 106 Potential.
FT TOPO_DOM 107 212 Extracellular (Potential).
FT TRANSMEM 213 233 Potential.
FT TOPO_DOM 234 253 Cytoplasmic (Potential).
FT CARBOHYD 127 127 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 152 152 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 167 167 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 183 183 N-linked (GlcNAc...) (Potential).
FT CONFLICT 85 85 Missing (in Ref. 4; AAH00704).
FT CONFLICT 236 236 R -> G (in Ref. 3; BAA91613).
SQ SEQUENCE 253 AA; 28018 MW; E074A4CD57229EC6 CRC64;
Alignment Scores:
Pred. No.: 2,29e-121 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 1 Gaps: 0

US-10-608-388a-1 (1-759) x TSN3_HUMAN (1-253)
QY 1 ATGGGCGAGTGGCGCATCTCTCCAAAGACCGTGGTGGTCTTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyIleThrSerSerIleThrValLeuValPheLeuAsnLeuIlePhe 20
QY 61 TGGGGGCGAGCTGGCATTTTATGCTATGTGGAGCCCTATGCTTTCATCCTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACACCTCTTTTGAAGATGTGTACACCTCATCTCTGCTGCTAGTGATCATGCTCTA 180
Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValIleAlaVal 60
QY 181 GGAGCCCTGCTTTTCATCTATGGGCTAAATGGCTGTGTGCCAATCCGGAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysAlaThrIleArgGluSerArg 80
QY 241 TGTGGACTGCCACGTTTGTGCATCATCTGCTCTTGGTTTGTGTCACAGAGTTGTTGTA 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
QY 301 GTGGTTTGGATATGTTTACAGAGCAAGGTGGAATGAGTTGATCGCAGCATTCAG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
QY 361 AAAGTGTATAGACTCAATGGAACCAACCTGATGCTAGCCGGGCTATTGATTAT 420
Db 121 LysValTyrLysThrThrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGAGACAGTGCATTTGTTGGAAATTCACAACTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
QY 481 TGGTTTCAAGAAACCAAAACAGAGTGTCCTCTTAGCTCTGCAGAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATGGCAGCTGGCCACCTTCCACCTCTATGCTAGGGGTGTGAGGCTCTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAGCTACAAGAAATCATGATGCATGTGATCTGGGCGGCACTGGCATTTGCA 660

| | | | | | |
|--------------|---|---|---------|--|--|
| Db | 161 | TrrPhelysGluThrIlysAenGlnSerValProLeuSerCysCysArgGluThrAlaIys | 180 | | |
| Qy | 541 | AAMTGTAAATGGCAGCTGGCCACCTTCGACCTCTATGCTGAGGGGTGTGAGGCTCTA | 600 | | |
| Db | 181 | SerCysAenGlySerLeuAlaAenProSerAspLeuTyrAlaGluGlyCysGluAlaLeu | 200 | | |
| Qy | 601 | GTACTGAAGAGCTACAGAATAATCATGATCCATGCTGATCTGGGCCGCACTGGCATTTGCA | 660 | | |
| Db | 201 | ValValIysLysLeuGlnGluLeuMetHisValIleTrrAlaLeuAlaIysPheAla | 220 | | |
| Qy | 661 | GCTATTACAGCTGCTGGGCATGCTGTGTGCTTGCATCTGTTGTGCAGAGGAGTAGAGAT | 720 | | |
| Db | 221 | AlaIleGlnLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp | 240 | | |
| Qy | 721 | CTTGCTTACAGCTCTCATCATCTGGCGGAACCTATGCA | 759 | | |
| Db | 241 | ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla | 253 | | |
| RESULT 4 | | | | | |
| Q545L1_MOUSE | | | | | |
| ID | Q545L1_MOUSE PRELIMINARY; | PRT; | 253 AA. | | |
| AC | Q545L1; | | | | |
| DT | 13-SEP-2005 (TrEMBLrel. 31, Created) | | | | |
| DT | 13-SEP-2005 (TrEMBLrel. 31, Last sequence update) | | | | |
| DT | 13-SEP-2005 (TrEMBLrel. 31, Last annotation update) | | | | |
| DE | Adult male testis cDNA, RIKEN full-length enriched library, full clone;1700055K04 product;transmembrane 4 superfamily member 8, full insert sequence (Tetraspanin). | | | | |
| GN | NamesTspan3; SynonymsTspan-3; | | | | |
| OS | Mus musculus (Mouse); | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; | | | | |
| OC | Muridae; Murinae; Mus. | | | | |
| OX | NCBI_TaxID=10090; | | | | |
| RN | [1] | | | | |
| RP | NUCLEOTIDE SEQUENCE. | | | | |
| RC | STRAIN=C57BL/6J; TISSUE=Testis; | | | | |
| RC | MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; | | | | |
| RC | Carninci P., Hayashizaki Y., | | | | |
| RT | "High-efficiency full-length cDNA cloning." | | | | |
| RT | Meth. Enzymol. 303:19-44 (1999). | | | | |
| RN | [2] | | | | |
| RP | NUCLEOTIDE SEQUENCE. | | | | |
| RC | STRAIN=C57BL/6J; TISSUE=Testis; | | | | |
| RC | MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500; | | | | |
| RC | Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., | | | | |
| RA | Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., | | | | |
| RA | Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., | | | | |
| RA | Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., | | | | |
| RA | Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavani T., | | | | |
| RA | Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., | | | | |
| RA | Kuehl P., Lewis S., Matsuo F., Nikaudo I., Pesole G., Quackenbush J., | | | | |
| RA | Schriml L.M., Straubli F., Suzuki R., Tonita M., Wagner L., Washio T., | | | | |
| RA | Sakai K., Okido T., Furuno M., Bono H., Baldarelli R., Barsh G., | | | | |
| RA | Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., | | | | |
| RA | Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., | | | | |
| RA | Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., | | | | |
| RA | Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., | | | | |
| RA | Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., | | | | |
| RA | Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., | | | | |
| RA | Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., | | | | |
| RA | Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., | | | | |
| RA | Hayashizaki Y.; | | | | |
| RT | "Functional annotation of a full-length mouse cDNA collection." | | | | |
| RT | Nature 409:685-690(2001). | | | | |
| RN | [3] | | | | |
| RP | NUCLEOTIDE SEQUENCE. | | | | |
| RC | STRAIN=C57BL/6J; TISSUE=Testis; | | | | |
| RC | MEDLINE=22354683; PubMed=12456851; DOI=10.1038/nature01266; | | | | |
| RC | Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., | | | | |
| RA | Okazaki I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., | | | | |
| RA | Nikaudo I., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., | | | | |
| RA | Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., | | | | |

RA Schriml L.M., Kanapin A., Matsuoka H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Bruscia V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrester A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kragg A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata K., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama S., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RA Tokoro Y., Shibuya K., Osawa M., Tahara-Hanaoka S., Iwama A.,
RA Kitamura T., Nakauchi H., Shibuya A.;
RT "Molecular Cloning and Characterization of mouse Tspan-3, A Novel
RT Member of the Tetraspanin Superfamily, Expressed on Resting.";
RL Biochem. Biophys. Res. Commun. 0:0-0 (2001).
DR EMBL; AK006798; BAB24745.1; -; mRNA.
DR EMBL; AB072450; BAB1751.1; -; mRNA.
DR MGI; MGI:1928098; Tspan3.

DR GO:0005615; C:extracellular space; TAS.
DR GO:0016021; C:integral to membrane; TAS.
KW Transmembrane.
SQ SEQUENCE 253 AA; 28048 MW; 8A7378F76263019A CRC64;
Alignment Scores:
Pred. No.: 6e-118 Length: 253
Score: 1301.00 Matches: 246
Percent Similarity: 98.4% Conservative: 3
Best Local Similarity: 97.2% Mismatches: 4
Query Match: 91.0% Indels: 0
DB: 2 Gaps: 0
US-10-608-388a-1 (1-759) x Q545L1_MOUSE (1-253)
QY 1 ATGGGCGAGTGGGCGATCACTCTCCAGACCGTCTGGTCTTTCTCAACCTCATCTTC 60
DB 1 MetGlyInCysGlylleThrSerSerLysThrValLeuValPheLeuAenLeullePhe 20
QY 61 TGGGGGCGAGCTGGGCAATTTTATGCTATGTGGGAGCCTATGTCTTTCATCATGTATGAC 120
DB 21 TrpGlyAlaAlaGlylleLeuCysTyrValGlyAlaTyrValPheilleThrTyrAspAsp 40
QY 121 TATGACCATCTTCTTGAAGATGTGTACGCTCATCCCTGCTGTAGTATCATGATCATGCTGA 180
DB 41 TyrAspHisPhePheGluAspValTyrThrLeuPheProAlaValValilleAlaVal 60
QY 181 GGAGCGCTCTTTTCATCATCTGGCTTAATGCTGCTGTGCCACATCCGGGAAGTCGC 240
DB 61 GlyAlaLeuLeuPheilleGlylleGlyCysAlaThrThrleArgGluSerArg 80
QY 241 TGTGGACTTGGCACCGTTTGTCTCATCTCTGCTCTTGGTCTTGTTCACAGAAAGTTGTGTA 300
DB 81 CysGlyLeuAlaThrPheValPheilleLeuLeuValPheValThrGluValValVal 100
QY 301 GTGGTTTTCGGATATGTTTACAGACAAAGGTGGAAATAGAGTTGATCGCAGATTTCAG 360
DB 101 ValValLeuGlyTyrValTyrArgAlaValGluValAspValArgSerileGln 120
QY 361 AAAGTGTATTAAGCACTTACATGGACCAACCTGATGCTGTAGCCGGCTATTGATTAT 420
DB 121 LysValTyrLysThrTyrAsnGlyThrAenSerAspAlaAlaSerArgAlaileAspTyr 140
QY 421 GTACAGAGACAGCTGCTGATTTGTGGAAATCAACACTCTACAGACTGGGAAAATACAGAT 480
DB 141 ValGlnArgGlnleuHisCysGlylleHisAsnTyrSerAspTrpGluAenThrAsp 160
QY 481 TGGTTCAAAGAAACCAAAACCAGAGTGTCCCTTTAGTGTGTCAGAGAGACTGCCAGC 540
DB 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaLys 180
QY 541 AATTGTATGGCAGCTGGCCACCCCTTCGACCTCTATGCTGAGGGGTGTAGGCTCTA 600
DB 181 SerCysAsnGlySerLeuAlaAenProSerAspLeuTyrAlaGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAACTCAAGAAATCATGATGCTATGCTGGGCCCATCTGGCATTGCA 660
DB 201 ValValLysLysGlnGlnleuLeuMetHisValleThrPalalaLeuAlaPheAla 220
QY 661 GCTATTACAGTCTGGGCAATGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 221 AlaileGlnLeuLeuGlyMetLeuCysAlaCysilleValLeuCysArgSerArgAsp 240
QY 721 CTGCTTACGAGCTCTCATCATCTGGCGGCACTATGCA 759
DB 241 ProAlaTyrGluLeuLeulleThrGlyGlyThrTyrAla 253
RESULT 5
Q66H05 RAT PRELIMINARY; PRT; 253 AA.
AC Q66H06;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Transmembrane 4 superfamily member 8.
GN Name=Tm4sf8;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
EC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Director MGC Project;
RA Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC082102; AAH82102.1; -; mRNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR000301; Transmem. 4.
DR Pfam; PF00335; Tetraspanin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
KW Transmembrane.
SQ SEQUENCE 253 AA; 28094 MW; 26B85FDDAP82ED8D CRC64;

Alignment Scores:
Pred. No.: 1.48e-117 Length: 253
Score: 1297.00 Matches: 245
Percent Similarity: 98.4% Conservative: 4
Best Local Similarity: 96.8% Mismatches: 4
Query Match: 90.8% Indels: 0
DB: 2 Gaps: 0

US-10-608-388A-1 (1-759) x Q6H06_RAT (1-253)

QY 1 ATGGSCCAGTGGGACATCCTCTCCAGACCGGTGCTTTCTCAACTCATCTTC 60
Db 1 MetGlyGlnCysGlyLeuThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
QY 61 TGGGGGGCAGCTGGCATTTTATGCTATGTGGGAGCGCTATGCTTCATCACTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyLeuLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACCACTTCTTTGAAGATGTGACACGCTCATCCCTGCTGTAGTCATCATCTGCTTA 180
Db 41 TyrAspHisPhePheGluAspValTyrThrLeuPheProAlaValValIleMetAlaVal 60
QY 181 GGAGCCCTCTTTTCATCATTTGGGCTAATGGCTGCTGTGGCCACATCGGGAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
QY 241 TGTGGACTTGGCCACGTTTGTGTCATCATCTCTGCTTCTTGGTTTGTGCACAGAAGTTGTTGA 300

Db 81 CysGlyLeuAlaThrPheValPheIleLeuLeuValPheValThrGluValValVal 100
QY 301 GTGGTTTGGGATATGTTTACAGAGCAAGTGGAAATGAGGTGATCGAGCATTCAG 360
Db 101 ValValLeuGlyTyrValTyrAlaLysValGluAsnGluAlaAspArgSerIleGln 120
QY 361 AAAGTGTATAGACCTTCAATAGGAACCAACCTGCTGCTAGCCGGGCTATTGATTAT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnSerAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGACAGCTGCATTTGTTGGAAATTCACAACTACTCAGACTGGGAAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTyrGluAsnThrAsp 160
QY 481 TGGTTCAAGAAACCAAAACCCAGAGTGCCTCTTAGCTGCTCAGACAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaArg 180
QY 541 AATTGTAAATGGCAGCTGGCCACCCCTTCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
Db 181 SerCysAsnGlySerLeuAlaAsnProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGACTACAGAAATCATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 201 ValValLysLysLeuGlnGluLeuMetHisValIleTrpAlaAlaLeuAlaPheAla 220
QY 661 GCTATTTCAGCTGCTGGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 240
QY 721 CCTGCTTACAGAGCTCTCATCACTGCGCGGAACCTATGCA 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

RESULT 6
Q80XR4 MOUSE
ID Q80XR4 MOUSE PRELIMINARY; PRT; 253 AA.
AC Q80XR4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Tetraspanin 3.
GN Name=Tspan3; Synonyms=Tm4sf8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

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RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RG NIH.MGC Project.
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC043072; AAH43072.1; -; mRNA.
DR Ensembl; ENSMUSG00000032324; Mus musculus.
DR MGI; MGI:1928098; Tm4sf8.
DR MGI; MGI:1928098; Tpan3.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspamin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; UNKNOWN 1.
SQ SEQUENCE 253 AA; 28148 MW; 9B6278F76263108B CRC64;

Alignment Scores:
Pred. No.: 3.63e-117 Length: 253
Score: 1293.00 Matches: 245
Percent Similarity: 98.0% Conservative: 3
Best Local Similarity: 96.8% Mismatches: 5
Query Match: 90.5% Indels: 0
DB: 2 Gaps: 0

US-10-608-388A-1 (1-759) x Q80XR4_MOUSE (1-253)

QY 1 ATGGGCGAGTGGCGCATCCTCTCCAGACCGTGGTCTTCTCAACCTCATCTTC 60
DB 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20

QY 61 TGGGGGCGAGTGGCATTTATGCTATGTGGGGACCTATGCTTCTCATCTTATGATGAC 120
DB 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrThrAspAsp 40

QY 121 TATGACCACTCTTTGAAGATGTGTACAGCTCATCCCTGCTGAGTGTGATCATAGTGTGA 180
DB 41 TyrAspHisPhePheGluAspValTyrThrLeuPheProAlaValIleIleAlaVal 60

QY 181 GGAGCCCTGCTTTTCATCATGGCTAATGGCTGCTGCCACAAATCCGGGAAGTCGC 240
DB 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysAlaThrIleArgGluSerArg 80

QY 241 TGTGGACTGCGAGTTGTTCATCATCTGCTGCTGTTGTTGTCACAGAGTTGTTGTA 300
DB 81 CysGlyLeuAlaThrPheValPheIleLeuLeuValPheValThrGluValVal 100

QY 301 GTGGTTTGGGATATGTTTACAGACAAAGTGGAAATGAGTTGATCCAGCATTCAG 360
DB 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120

QY 361 AAGTGTATAGACCTACATGAGNACCAACCGCTGATCTGCTAGCCGGCTATTGATTAT 420
DB 121 LysValTyrLysThrTyrAsnGlyThrAsnSerAspAlaAlaSerArgAlaIleAspTyr 140

QY 421 GTACAGACAGCTGCATTGTTGGGAATTCACAACTACTCAGACTCGGAAATACAGAT 480
DB 141 ValGlnArgGlnLeuHisCysCysArgIleHisnTyrSerAspTrpGluAsnThrAsp 160

QY 481 TGGTTCAAGAAACCAAAAAACAGAGTGTCCCTCTTAGCTGCTGCAGAGACTGCCAGC 540
DB 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaLys 180

QY 541 AATTGTAAATGGAGCTGGCCGCCCTTCGACCTCTATGCTGAGGGGTGTAGGCTCTA 600
DB 181 SerCysAsnGlySerLeuAlaAsnProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200

QY 601 GTAGTGAAGAGCTACAGAAATCATCATGTCATGCTGGCGGACCTGGCATTTGCA 660
DB 201 ValValLysLeuGlnGluIleLeuWechisValIleTrpAlaAlaLeuAlaPheAla 220

QY 661 GCTATTGAGTGGCGATGCTGTGCTTGTGATCGTGTGTCAGAGGAGTAGAGAT 720

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Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
QY 721 CCTGCTTAGAGCTCTCTCATCTGCGGACCACTATGCA 759
Db 241 ProAlaTyrGlnLeuLeuIleThrGlyThrTyrAla 253

RESULT 7
Q4V915_BRARE PRELIMINARY; PRT; 253 AA.
ID Q4V915_BRARE PRELIMINARY; PRT; 253 AA.
AC Q4V915_2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein MGC114050.
GN Names:MGC114050;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Larvae;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Heiton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Larvae;
RG NIH MGC Project;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC097114; AAH97114.1; -; mRNA.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspamin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 253 AA; 28203 MW; F4DCB5557E2B8D78 CRC64;

Alignment Scores:
Pred. No.: 1.03e-106 Length: 253
Score: 1186.00 Matches: 221
Percent Similarity: 92.5% Conservative: 13
Best Local Similarity: 87.4% Mismatches: 19
Query Match: 83.0% Indels: 0
DB: 2 Gaps: 0

US-10-608-388A-1 (1-759) x Q4V915_BRARE (1-253)

QY 1 ATGGGCGAGTGGCGCATCCTCTCCAGACCGTGGTCTTCTCAACCTCATCTTC 60
DB 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20

QY 61 TGGGGGCGAGTGGCATTTATGCTATGTGGGGACCTATGCTTCTCATCTTATGATGAC 120

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| | | | |
|----|-----|---|-----|
| Qy | 541 | AATTGTAATGCGAGCTGGCCACCCTTCGACCTCTATGCTGAGGGGTGAGGCTCTA | 600 |
| Db | 181 | AsnCysThrGlySerMetAsnLysProGluAspLeuTy-SerGluGlyCysGluAlaLeu | 200 |
| Qy | 601 | GTAGTGAAGNAGCTACAGAAATCATGATGCATGTCATCGGCGCCGACCTGGCATTTGCA | 660 |
| Db | 201 | ValValGluGluLeuGlnGlnIleMetMetTyValIleTrpAlaAlaLeuAlaPheAla | 220 |
| Qy | 661 | GCTATTACGCTCTGGGACATGCTGTGTGCTGTGTCATCGTCTTGTGCAGAGGAGTAGAGAT | 720 |
| Db | 221 | ThrIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuLeuCysArgArgThrArgAsp | 240 |
| Qy | 721 | CTGTGCTTACGAGCTCTCATCACTGGCGGAACCTATGCA | 759 |
| Db | 241 | ProAlaTyGluLeuLeuIleThrGlyGlyThrTyAla | 253 |

RESULT 9

Q5XH66 XENLA

ID Q5XH66 XENLA PRELIMINARY; PRT; 253 AA.

AC Q5XH66;

DT 25-OCT-2004 (TREMBLrel. 28, Created)

DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)

DE LOC495251 protein.

GN Name=LOC495251;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus; Xenopus.

OX NCBI_taxid=8355;

ON [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Ovary;

RE MEDLINE=223841132; PubMed=12454917; DOI=10.1002/dvdy.10174;

RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

RA Richardson P.;

RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus

RT initiative";

RL Dev. Dyn. 225:384-391 (2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Ovary;

RE MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Vallation D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Ovary;

RE Klein S., Gerhard D.S.;

RL Submitted (OCT-2004) to the EMBL/GenBank/DBSJ databases.

DR EMBL; BC084207; AA084207.1; -; mRNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR InterPro; IPR000301; Transmem 4.

DR Pfam; PF00335; Tetraspanin; I.

121 LysValTyrAsnGluTyrAsnGlyThrAsnSerAspAlaProSerArgAlaIleAspTyr 144

421 GTACAGACAGCTGCATCTTTGTGGAATTCACAACCTACTCAGACTGGGAAATAATACAGAT 480

141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTyrArgAsnThrArg 160

481 TGGTTCACAAAGAACCAACCAACAGAGTGTCCTCTAGCTGCTGCAGAGAGACTGCCAGC 540

161 TrpPheLysGluSerArgAsnAsnSerValProValSerCysGlnProSerIleSer 180

541 AATTTGTAATGGCAGCTGGCGCCACCCCTTCGAGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600

181 AsnCysThrGlyThrLeuAlaAArgProSerGluLeuTyrGlnGluGlyCysGluAlaLeu 200

601 GTAGTGAAGAAGCTTACAAGAAATCATGATGCATGTGATCTGGCGCGCACTGGCATTTGCA 660

201 ValValLysLysLeuLysGluIleMetMetTyrValIleTrpAlaAlaLeuThrPheAla 220

661 GCTATTTCAGCTGTGGGCATGCTGTGCTGTGCATCTGTTGTCAGAGAGAGTAGAGAT 720

221 SerIleGlnMetLeuGlyMetLeuCysAlaCysValValLeuCysArgArgThrHisasp 240

721 CCTGCTTACAGAGTCCCTCATCCTACCTGGCGGGAACCTATGCA 759

241 ProAlaTyrGluLeuLeuValThrAsnSerTyrAla 253

RESULT 11

Q8BP2_MOUSE

ID Q8BP2_MOUSE PRELIMINARY; PRT; 245 AA.

AC Q8BP2_MOUSE (23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:B13009003 product:transmembrane 4 superfamily member 8, full insert sequence.

DE Name:Trp3n3; Synonym:Trm4sf8; .

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP [1]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=EyeBall;

RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RP [2]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=EyeBall;

RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itch M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staebli P.F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seyga T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

Db 220 PhePheGlyMetLeuSerValCysValIleThrCysLysSerLysLysAsnGluTyrGln 239

QY 721 CTGCTTAC 729
||| |||
Db 240 ProLeuTyr 242

RESULT 15

Q6GP11_XENLA PRELIMINARY; PRT; 240 AA.

AC Q6GP11;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE MGC80751 protein.
GN Name=MGC80751; (African clawed frog).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stabileton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lomuellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Bailey M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073338.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspannin; I.
DR PRINTS; PRO0259; TMFOUR.
SQ SEQUENCE 240 AA; 26875 MW; 96475F0A8F920998 CRC64;

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 2,19e-42 | Length: | 240 |
| Score: | 527.50 | Matches: | 89 |
| Percent Similarity: | 62.8% | Conservative: | 61 |
| Best Local Similarity: | 37.2% | Mismatches: | 84 |
| Query Match: | 36.9% | Indels: | 5 |
| DB: | 2 | Gaps: | 3 |

US-10-608-388A-1 (1-759) x Q6GP11_XENLA (1-240)

QY 22 TCCTCCAGACGGCTGGTCTTCTCAACTCATCTTCTGGGGGACAGCTGGCATTTTA 81
:::|||||
Db 7 ThrSerLysThrPheLeuValSerLeuIlePheLeuAlaAlaSerValGlyLeu 26
:::|||||
QY 82 TGCTATGTGGAGGCTATGCTTCATCATTATGATGACTATGACCACTTCTTTGAAGAT 141
|||||
Db 27 AlaTyrValGlyIleSerThrIleValThrTyrLysGlnTyrGluAspLeuGlyAsn 46
|||||
QY 142 GTGTACAGCTCATCCCTGCTGTAGTATGATCATAGCTGTAGGAGCCCTCTCTTCATCAT 201
:::|||||
Db 47 MetTyrValMetLeuProSerValIleIleLeuAlaIleValIleValMetPhePhe 66
:::|||||
QY 202 GGGCTAATTGGCTGCTGGCCACAAATCGGGAAGTCTGCTGACCTTGCCACGTTTGTG 261
:::|||||
Db 67 AlaIleLeuGlyCysSerThrThrGlnGluSerCysGlyLeuGlyCysPheMet 86
:::|||||
QY 262 ATCATCTGCTCTTGGTGTTCACAGAACTGTGTGTAGTGGTGTGGGATATGTTTAC 321
:::|||||
Db 87 PheLeuIleSerIleIlePheAlaAlaGlyValAlaAlaIleIleLeuGlyLeuValTyr 106
:::|||||
QY 322 AGAGCAAGGTGGAAATGAGGTGTATCGCAGCATTCAGAAAGTGTATAGACCTACAT 381
:::|||||
Db 107 ValAsnLysIleAsnProGluLeuGluLysAsnMetAspAsnLeuTyrLysLysTyrSer 126
:::|||||
QY 382 GGAACCAACCTGATGCTGTAGCCGGCTATTGATTATGTACAGACAGACAGCTGCTATTGT 441
:::|||||
Db 127 GlyAla-----AppValGlnSerThrValAspPheIleGlnGluLeuGlnCys 144
:::|||||
QY 442 TGTGGAATTCACAACTACTCAGACTGGGAAATACAGATTGTTTCAAAAGAACCAAAAC 501
:::|||||
Db 145 CysGlyArgLysAsnTyrThrAspTyrGluGluThrAspTyrTyrLys-----AsnAsn 162
:::|||||
QY 502 CAGAGTGTCCCTCTTGTAGCTGTGAGAGAGACTGCCAGCAATTGTATGGCAGCTGSCC 561
:::|||||
Db 163 LysSerLeuProLeuSerCysCysLysLysAsnAlaGlnAspCysGlnArgValIleGly 182
:::|||||
QY 562 CACCTTCGACCTCTATGCTGAGGGGTGTGAGGCTCTAGTAGTGAAGAAGCTACAAGAA 621
:::|||||
Db 183 GlnIleLysAspIleTyrThrGluGlyCysGluProLysLeuGluThrLeuIleHisGln 202
:::|||||
QY 622 ATCATGTGATGTGATCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 681
:::|||||
Db 203 ValLeuArgTyrSerMetPheValIleLeuGlyPheAlaIleValGluLeuPheAlaMet 222
:::|||||
QY 682 CTGTGCTTGCATCGTGTGTGAGAGAGAGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTC 738
:::|||||
Db 223 IleSerMetCysValIleSerCysArgProAlaArgHis---ThrTyrHisLeuLeu 240
:::|||||

Search completed: April 4, 2006, 21:31:38
Job time : 230 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 4, 2006, 21:24:24 ; Search time 8.1 Seconds
(without alignments)
1803.173 Million cell updates/sec

Title: US-10-608-388A-1

Perfect score: 1429

Sequence: 1 atgggccagcgcgccatcac.....tcactggcggaacctatgca 759

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlip
-Q=/abss/ABSSWEB_spool/US10608388/runat_04042006_150651_14080/app_query.fasta_1
-DB=PIR -QMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02p
-USER=US10608388 @CGN_1_1_63 @runat_04042006_150651_14080 -NCPUS=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 1336 | 93.5 | 253 | 2 A59264 | tetraspan TSPAN-3 |
| 2 | 343.5 | 24.0 | 244 | 1 I39368 | T-cell acute lymph |
| 3 | 333.5 | 23.3 | 245 | 2 A59258 | tetraspan TSPAN-6 |
| 4 | 333.5 | 23.3 | 245 | 2 A59260 | tetraspan TSPAN-6 |
| 5 | 330.5 | 23.1 | 238 | 1 S43511 | CD63/ME491 antigen |
| 6 | 328.5 | 23.0 | 238 | 1 A46508 | CD63 antigen |
| 7 | 322.5 | 22.6 | 238 | 1 JC2297 | CD63 antigen - rab |
| 8 | 301.5 | 21.1 | 238 | 2 A59265 | tetraspan TSPAN-4 |
| 9 | 297.5 | 20.8 | 238 | 1 I38016 | melanoma-associate |
| 10 | 283 | 19.8 | 267 | 1 A46493 | metastasis suppress |
| 11 | 273.5 | 19.1 | 219 | 1 A37243 | hemopoietic cell s |
| 12 | 263 | 18.4 | 241 | 2 A59262 | tetraspan TSPAN-1 |
| 13 | 259.5 | 18.2 | 219 | 1 A39574 | leukocyte antigen |
| 14 | 259.5 | 18.2 | 266 | 2 I49561 | C33/R2/IA4 - mouse |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 15 | 257.5 | 18.0 | 281 | 1 B47629 | cell surface glyco |
| 16 | 251 | 17.6 | 218 | 1 A40181 | 23K integral membr |
| 17 | 251 | 17.6 | 237 | 1 A36056 | tumor-associated a |
| 18 | 250.5 | 17.5 | 282 | 2 T21896 | hypothetical prote |
| 19 | 242.5 | 17.0 | 281 | 1 A47629 | cell surface glyco |
| 20 | 235 | 16.4 | 218 | 1 A43522 | 23K integral membr |
| 21 | 222.5 | 15.6 | 226 | 1 JX0221 | CD9 antigen - bovi |
| 22 | 218.5 | 15.3 | 226 | 1 S39262 | CD9 antigen - rat |
| 23 | 218.5 | 15.3 | 226 | 2 I49589 | antigen - mouse |
| 24 | 218.5 | 15.3 | 228 | 1 A40402 | CD9 antigen (valid |
| 25 | 215.5 | 15.1 | 228 | 1 A42929 | CD9 antigen - gree |
| 26 | 210 | 14.7 | 206 | 2 T25161 | hypothetical prote |
| 27 | 207.5 | 14.5 | 236 | 1 A46472 | cell surface prote |
| 28 | 205 | 14.3 | 222 | 2 A59263 | tetraspan TSPAN-2 |
| 29 | 201.5 | 14.1 | 236 | 1 A35649 | cell surface prote |
| 30 | 196 | 13.7 | 308 | 2 T24912 | hypothetical prote |
| 31 | 183.5 | 12.8 | 264 | 2 A59261 | tetraspan TSPAN-5 |
| 32 | 182.5 | 12.8 | 194 | 2 T25548 | hypothetical prote |
| 33 | 174 | 12.2 | 233 | 2 T15620 | hypothetical prote |
| 34 | 171 | 12.0 | 359 | 2 T18667 | hypothetical prote |
| 35 | 164 | 11.5 | 427 | 2 T32852 | hypothetical prote |
| 36 | 159 | 11.1 | 321 | 2 T45053 | hypothetical prote |
| 37 | 155.5 | 10.9 | 242 | 2 T15361 | hypothetical prote |
| 38 | 153 | 10.7 | 203 | 2 T22537 | hypothetical prote |
| 39 | 151.5 | 10.6 | 351 | 2 I54347 | rod outer segment |
| 40 | 149 | 10.4 | 258 | 2 I46080 | uroplakin Ia - bov |
| 41 | 143 | 10.0 | 260 | 2 A41531 | TGFbeta-regulated |
| 42 | 138 | 9.7 | 172 | 2 T28914 | hypothetical prote |
| 43 | 137 | 9.6 | 260 | 2 I46081 | uroplakin Ib - bov |
| 44 | 137 | 9.6 | 702 | 2 T34313 | hypothetical prote |
| 45 | 133.5 | 9.3 | 366 | 2 T22544 | hypothetical prote |

ALIGNMENTS

RESULT 1

A59264
tetraspan TSPAN-3 - human
C:Species: Homo sapiens (man)
C:Date: 13-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A59264
R:Todd, S.C.; Doctor, V.S.; Levy, S.
Biochim. Biophys. Acta 1399, 101-104, 1998
A:Title: Sequences and expression of six new members of the tetraspanin/TW4SF family.
A:Reference number: A59258; MUID:98390278; PMID:9714763
A:Accession: A59264
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-253 <TOD>
A:Cross-references: UNIPROT:O60637; UNIPARC:UPI0000048A5D; GB:AF054840; NID:G2997744;
C:Gene: TSPAN-3
C:Superfamily: CD9 antigen

Alignment Scores:
Pred. No.: 4.39e-118 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 2 Gaps: 0

US-10-608-388A-1 (1-759) x A59264 (1-253)

| | | | |
|----|-----|--|-----|
| QY | 1 | ATGGGCCAGTGGGCGCATCCCTCCCAAGACCGTGGTCTCTTCTCAACCTCATCTTC | 60 |
| | | | |
| DB | 1 | MetGlyGlnCysGlyIleThrSerSerLyThrValLeuValPheLeuLeuLeuPhe | 20 |
| QY | 61 | TGGGGGGGAGCTGGCGATTTATGCTATGTGGGAGCCTATGCTTTCATCATATGATGAC | 120 |
| | | | |
| DB | 21 | TTPGlyAlaAlaGlyIleLeuLeuCysTrValGlyAlaTrValPheIleThrTrAspAsp | 40 |
| QY | 121 | TATGACCACTTCTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTCATAGCTGTA | 180 |

QY 556 CTGGCCACCCCT-----TCCGACCTCTATGCTGAGGGGTGTGAGGCTCTAGTA 603
 DB 184 -----TyrProGlnArgAspAlaAspLysValaGluGluGlyCysPheIleIysVal 201
 QY 604 GTGAAGAAGCTACAAAGAAATCATGATGATGATGCTGGGGCGGCACCTGGCATTTGCGACT 663
 DB 202 MetThrThrIleGluSerGluMetGlyValValAlaGlyIleSerPheGlyValAlaCys 221
 QY 664 ATTGAGCTGCTGGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
 DB 222 PheGlnLeuIleGlyPheLeuAla---TyrCysLeuSerArgAlaIleThrAsnAsn 240
 QY 724 GCTTACGAGCTCCTC 738
 DB 241 GlnTyrGluIleVal 245

RESULT 5
 S43511
 CD63/ME491 antigen homolog - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
 C:Accession: S43511
 R:Miyaoto, H.; Homma, M.; Hotta, H.
 Biochim. Biophys. Acta 1217, 312-316, 1994
 A:Title: Molecular cloning of the murine homologue of CD63/ME491 and detection of its s
 A:Reference number: S43511; MUID:94198294; PMID:8148377
 A:Accession: S43511
 A:Molecule type: mRNA
 A:Residues: 1-238 <MI>
 A:Cross-references: UNIPROT:P41731; UNIPARC:UPI00000002B1; EMBL:D16432; NID:9484052; PID
 C:Superfamily: CD9 antigen
 C:Keywords: glycoprotein; lysosome; surface antigen; transmembrane protein
 F:1-11/Domain: intracellular #status predicted <CY1>
 F:12-35/Domain: transmembrane #status predicted <TM1>
 F:36-51/Domain: extracellular #status predicted <EX1>
 F:52-76/Domain: transmembrane #status predicted <TM2>
 F:77-80/Domain: intracellular #status predicted <CY2>
 F:81-103/Domain: transmembrane #status predicted <TM3>
 F:104-202/Domain: extracellular #status predicted <EX2>
 F:203-228/Domain: transmembrane #status predicted <TM4>
 F:229-238/Domain: intracellular #status predicted <CY3>
 F:116,130,150,172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
 Pred. No.: 5 1e-23 Length: 238
 Score: 330.50 Matches: 79
 Percent Similarity: 53.7% Conservative: 51
 Best Local Similarity: 32.6% Mismatches: 103
 Query Match: 23.1% Indels: 9
 DB: 1 Gaps: 5

US-10-608-388A-1 (1-759) x S43511 (1-238)

QY 13 GGCATCACCTCTCCAGACCGTGTGCTGCTTCTCAACCTCATCTCTCGGGGGGACGT 72
 DB 6 GlyMetLysCysValLysPheLeuLeuTyrValLeuLeuLeuAlaPheCysAlaCysAla 25
 QY 73 GGCATTTATGCTATGCTGGGAGCCTATGCTTTCATCATCTTATGATGATGATGACCACTTC 132
 DB 26 ValGlyLeuIleAlaIleGlyValAlaValGlnValValLeuLysGlnAlaIleThrHis 45
 QY 133 TTGAGATGTGTACACCTCATCTCTGCTAGTATCATAGCTGTAGGAGCCCTGTT 192
 DB 46 GluThrThrAlaGlySerLeuLeuPro---ValValIleIleAlaValGlyAlaPheLeu 64
 QY 193 TTCATCATGGGCTAATTGGTGTGCTGCCCAATCCGGGAAGTCGCTGTGGACTGCC 252
 DB 65 PheLeuValAlaPheValGlyCysGlyAlaCysLysGluAsnTyrCysLeuMetile 84
 QY 253 ACGTTTGTATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 312
 DB 85 ThrPheAlaIlePheLeuSerLeuIleMetLeuValGluValAlaValAlaIleAlaGly 104

QY 313 TATGTTTACAGACAAAGTGGAAATGAGGTTGATCGCAGCATTCAGAAAGTGTATAAG 372
 DB 105 TyrValPheArgAspGlnValLysSerGluPheAsnLysSerPheGlnGlnMetGln 124
 QY 373 ACCTACATGGAACCAACCCCTGATGCTGCTAGCCGGGCTATTGATTATGTACAGACAG 432
 DB 125 AsnTyrLeuLysAspAsnLysThrAlaThr-----IleLeuAspLysLeuGlnLysGlu 142
 QY 433 CTGCATTGTTGTGAATTCACACTACTCAGACTGGGAAATACAGATTGGTTCAAAGAA 492
 DB 143 AsnAsnCysCysGlyAlaSerAsnTyrThrAspTrpGluAsnIleProGlyMetAlaLys 162
 QY 493 ACCAAACACAGAGTGTCCCTCTTGTGCTGTCAGAGAGACTGCCAGCAATTTGTAATGGC 552
 DB 163 AspArg-----ValProAspSerCysCysIleAsnIleThrValGlyCys---Gly 178
 QY 553 AGCTGCGCCACCCCTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTAGTAGTGAAGA 612
 DB 179 AsnAspPheLysGluSerThrIleHisThrGlnGlyCysValGluThrIleAlaIleTrp 198
 QY 613 CTCAAGAAATCATGATGATGATGCTGGCGGCGCACTTGCAGCTATTTCAGCTG 672
 DB 199 LeuArgLysAsnIleLeuValAlaAlaAlaLeuGlyIleAlaPheValGluVal 218
 QY 673 CTGGCGATGCTGTGTGCTTCATGCTGCTGTCAGAGAGAGTAGAGATCCCTGCTTACGAG 732
 DB 219 LeuGlyIleIlePheSerCysLeuVal-----LysSerIleArgSerGlyTyrGlu 236
 QY 733 CTCCTC 738
 DB 237 ValMet 238

RESULT 6
 A46508
 CD63/ME491 antigen homolog - rat
 N:Alternate names: mast cell antigen AD1
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 18-Jun-1993 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
 C:Accession: A46508; S16776
 R:Nishikata, H.; Oliver, C.; Mergenhagen, S.E.; Siraganian, R.P.
 J. Immunol. 149, 862-870, 1992
 A:Title: The rat mast cell antigen AD1 (homologue to human CD63 or melanoma antigen ME:
 A:Reference number: A46508; MUID:92340890; PMID:1634775
 A:Accession: A46508
 A:Molecule type: mRNA
 A:Residues: 1-238 <NTS>
 A:Cross-references: UNIPROT:P28648; UNIPARC:UPI0000167A7D; EMBL:X61654; NID:955601; PU
 A:Note: This antigen was found localized to mast cells in tissue samples, but was induc
 A:Note: sequence extracted from NCBI backbone (NCBI:109346, NCBI:P:109349)
 C:Comment: This heavily glycosylated protein of 50-60K (27K after deglycosylation) is
 C:Superfamily: CD9 antigen
 C:Keywords: glycoprotein; lysosome; mast cell; surface antigen; transmembrane protein
 F:1-11/Domain: intracellular #status predicted <CY1>
 F:12-35/Domain: transmembrane #status predicted <TM1>
 F:36-51/Domain: extracellular #status predicted <EX1>
 F:52-76/Domain: transmembrane #status predicted <TM2>
 F:77-80/Domain: intracellular #status predicted <CY2>
 F:81-103/Domain: transmembrane #status predicted <TM3>
 F:104-202/Domain: extracellular #status predicted <EX2>
 F:203-228/Domain: transmembrane #status predicted <TM4>
 F:229-238/Domain: intracellular #status predicted <CY3>
 F:130,150,172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
 Pred. No.: 7.88e-23 Length: 238
 Score: 328.50 Matches: 79
 Percent Similarity: 52.5% Conservative: 48
 Best Local Similarity: 32.6% Mismatches: 106
 Query Match: 23.0% Indels: 9
 DB: 1 Gaps: 5

US-10-608-388A-1 (1-759) x A46508 (1-238)

C/Species: Homo sapiens (man)
C/Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C/Accession: A59265
R/Todd, S.C.; Doctor, V.S.; Levy, S.
Biochim. Biophys. Acta 1399, 101-104, 1998
A/Title: Sequences and expression of six new members of the tetraspanin/TW4SF family.
A/Reference number: A59258; MUID:98390278; PMID:9714763
A/Accession: A59265
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-238 <TOD>
A/Cross-references: UNIPROT:O14817; UNIPARC:UPI000013683F; GB:AF054841; NID:92997746;
C/Genetics:
A/Gene: TSPAN-4
C/Superfamily: CD9 antigen

```

Alignment Scores:
Pred. No.:      2,81e-20      Length:      238
Score:          301.50       Matches:      72
Percent Similarity: 47.5%    Conservative: 44
Best Local Similarity: 29.5% Mismatches:      119
Query Match:    21.1%       Indels:        9
DB:              2          Gaps:         4

US-10-608-388A-1 (1-759) x A59265 (1-238)

Qy      1  ATGGGCCAGTGGCGGATCACCTCTCCACAGCGTGGTCTTTCTCAACCTCATCTTC 60
      |||  : : : : : |||  : : : : : |||  : : : : : |||
Db      1  MetAlaArgAlaCysLeuGlnAlaValIysTyrLeuMetPheAlaPheAsnLeuLeuPhe 20
      |||  : : : : : |||  : : : : : |||  : : : : : |||
Qy     61  TGG---GGGGCAGCTGGGCATTTTATGCTATGPGGGAGCCCTATGCTTTCATCACTTATGAT 117
      |||  : : : : : |||  : : : : : |||  : : : : : |||

```

| | | | | |
|-----|--|-----|--|-----|
| Db | | 21 | TrpLeuGlyGlyCysGlyValLeu---GlyValGlyIleTrpLeuAlaAlaThrGlnGly | 39 |
| QY | | 118 | GACTATGACCACTTCTTTGAGAGATGTTACAGCGCTCATCCCTGCTGTAGTCAATCATAGCT | 177 |
| Db | | 40 | SerPheAlaThrLeuSer-SerSerPheProSerLeuSerAlaAlaAsnLeuLeuIle | 59 |
| .QY | | 178 | GTAGGAGCGCTGCTTTTCATCATTTGGGTAAATTGGCTGCTGTGCCACAATCCGGAAAGT | 237 |
| Db | | 60 | ThrGlyAlaPheValMetAlaIleGlyPheValGlyCysLeuGlyAlaIleLysGluAsn | 79 |
| QY | | 238 | CGCTGTGGACHTGGCCAGCTTGTCTCATCATCTCGCTCTCTGGCTTTTGTCCACAGAAGTTGTT | 297 |
| Db | | 80 | LysCysLeuLeuLeuThrPhePheLeuLeuLeuLeuValPheLeuLeuGluAlaThr | 99 |
| QY | | 298 | GTAGTGGTTTGGGATATGTTTACAGACCAAGGTGGAAAATGAGGTTGATCGCAGCATT | 357 |
| Db | | 100 | IleAlaIleLeuPhePheAlaTyrThrAspLysIleAspArgTyrAlaGlnGlnAspLeu | 119 |
| QY | | 358 | CAGAAAGTGTATAGACCTACAAATGGAAACCAACCCGTGCTGTAGCGGGCTATTGAT | 417 |
| Db | | 120 | LysLysGlyLeuHisLeuTyrGlyThrGlnGlyAsnValGlyLeuThrAsnAlaTrpSer | 139 |
| QY | | 418 | TATGTACAGACAGACTGCATTGTTGTGGAATTCACAACTACTACAGACTGGGAAATACA | 477 |
| Db | | 140 | IleIleGlnThrAspPheArgCysGlyValSerAsnTyr-----Thr | 154 |
| QY | | 478 | GATTGTTTCAAGAAACCAAAAACAGAGTGTCCCTCTTAGCTGTGCAGAGACTGCC | 537 |
| Db | | 155 | AspTrpPheGluValTyrAsnAlaThrArgValProAspSerCysCysLeuGluPheSer | 174 |
| QY | | 538 | AGCAATTCTAATGGCAGCTGSCCCACCTTCCGACCTCTATGCTGAGGGGTGTGAGGCT | 597 |
| Db | | 175 | GluSerCys-----GlyLeuHisAlaProGlyThrTrpTrpLysAlaProCysTyrGlu | 192 |
| QY | | 598 | CTAGTAGTGAAGAGCTACAAGAAATCATGATGCATGTGCGCCGCACATGGCATTT | 657 |
| Db | | 193 | ThrValLysValTrpLeuGlnGluAsnLeuLeuAlaValGlyIlePheGlyLeuCysThr | 212 |
| QY | | 658 | GCAGCTATTCAGCTCTGGGCATGCTGTGTGCTTGCATCGTGTGTGCAGAGAGGTAGA | 717 |
| Db | | 213 | AlaLeuValGlnIleLeuGlyLeuThrPheAlaMetThrMetTyrCysGlnValLys | 232 |

C;Genetics:
A;Gene: GDB:CD63; MLA1
A;Cross-references: GDB:I20186; OMIM:155740
A;Map position: 12q12-12q13
A;Introns: 22/3; 85/3; 110/3; 142/3; 189/3; 217/3
C;Superfamily: CD9 antigen
C;Keywords: Glycoprotein; lysosome; surface antigen; transmembrane protein
F;2-238/Product: melanoma-associated antigen ME491 #status experimental <M>
F;2-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <EX1>
F;36-51/Domain: extracellular #status predicted <EX1>
F;52-76/Domain: transmembrane #status predicted <EX2>
F;77-80/Domain: intracellular #status predicted <CY2>
F;81-103/Domain: transmembrane #status predicted <EX3>
F;104-202/Domain: extracellular #status predicted <EX3>
F;203-228/Domain: transmembrane #status predicted <EX4>
F;229-238/Domain: intracellular #status predicted <CY3>
F;130,150,172/Binding site: carbohydrate (Asn) #status predicted

Alignment Scores:
Pred. No.: 6.72e-20 Length: 238
Score: 297.50 Matches: 79
Percent Similarity: 50.4% Conservative: 48
Best Local Similarity: 31.3% Mismatches: 96
Query Match: 20.8% Indels: 29
DB: 1 Gaps: 9

US-10-608-388A-1 (1-759) x I38016 (1-238)

QY 13 GGATCATCCTCTCCAGACCGTCTGCTTTCTCAACCTCATCTTCTGGGGG---GCA 69
Db 6 GlyMetLysCysValLysPheLeuLeuTyrrValLeuLeuAlaPheCysAlaCysAla 25
QY 70 GCTGGCATTTTATGCTAT---GTGGGAGCTATGCTTCTCATCATGATGATGATGAC 126
Db 26 ValGlyLeuLeuAlaValGlyValGlyAlaGlnLeuValLeuSer----- 40
QY 127 CACTTCTTTGAAGATGTGTACAGCTCATCTCCCTGCT----- 162
Db 41 -----GlnThrIleIleGlnGlyAlaThrProGlySerLeuLeuPro 54
QY 163 GTATGATCATAGCTGTAGAGCGCTGCTTTTTCATCATTTGGGTAAATGGCTGCTGTC 222
Db 55 ValValIleIleAlaValGlyValPheLeuPheLeuValAlaPheValGlyCysGly 74
QY 223 ACAATCGGGAAGTGCCTGTGACCTGCCAGCTTGTCTATCATCTGCTCTTGGTTTTT 282
Db 75 AlaCysLysGluAsnTyrrCysLeuMetIleThrPheAlaIlePheLeuSerLeuMet 94
QY 283 GTCACAGAAGTGTGTAGTGGTGTGGATATGTTTACAGACCAAGGTGGAATATGAG 342
Db 95 LeuValGluValAlaAlaAlaIleAlaGlyTyrrValPheArgAspLysValMetSerGlu 114
QY 343 GTTGATCGACATTCAGAAAGTGTATPAGACCTTACAACTGGAACCACTGATGCTGCT 402
Db 115 PheAsnAsnAsnPheArgGlnMetGluAsnTyrrProLysAsnAsnHisThrAlaSer 134
QY 403 AGCGGGCTATTGATATGTATGATACAGACACAGCTGCATGTTGTGGATTTCACACTCA 462
Db 135 -----IleLeuAspArgMetGlnAlaAspPheLysCysGlyAlaAlaAsnTyrrThr 152
QY 463 GACTTGGGAAATACAGATGTTTCAAGAAACCAAAACAGAGTGTCCCTCTTAGCTGC 522
Db 153 AspIrrpGluLysIlePro-----SerMetSerLysAsnArg---ValProAspSerCys 169
QY 523 TGCAGAGAGACTGCCAGCAATTTGTAATGGAGCGCTGGCCCACTTCCGACCTCTATGCT 582
Db 170 CysIleAsnValThrValGlyCys---GlyIleAsnPheAsnGluLysAlaIleHisLys 188
QY 583 GAGGGGTGAGGCTCTAGTAGTGAAGAACTACAGAAATCATGATGATGATGATGCTGG 642
Db 189 GluGlyCysValGluLysIleGlyGlyTrpLeuArgLysAsnValLeuValAlaAla 208

QY 643 GCGCACTGGCATTTGCACTATTCAGCTGCTGGCATGCTGTGCTGCTGCTGCTGTTG 702
Db 209 AlaAlaLeuGlyIleAlaPheValGluValLeuGlyIleValPheIlaCysCysLeuVal 228
QY 703 TGCAGAAAGAGTAGATGATCTGCTTTACGAGCTCCTC 738
Db 229 -----LysSerIleArgSerGlyTyrrGluValMet 238
RESULT 10
A46493
metastasis suppressor KAI1 - human
N;Alternate names: cell surface glycoprotein KAI1; membrane protein R2, inducible; ty
C;Species: Homo sapiens (man)
C;Date: 18-Jun-1993 #sequence revision 09-Aug-1996 #text_change 09-Jul-2004
C;Accession: I38942; S16156; A46493
R;Dong, J.T.; Lamb, P.W.; Rinker-Schaeffer, C.W.; Vukanovic, J.; Ichikawa, T.; Isaacs, S.
Science 288, 884-886, 1995
A;Title: KAI1, a metastasis suppressor gene for prostate cancer on human chromosome 1:
A;Reference number: I38942; MUID:95273964; PMID:7754374
A;Accession: I38942
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-267 <RES>
A;Cross-references: UNIPROT:P27701; UNIPARC:UPI00001273AE; EMBL:U20770; NID:9806805; I
R;Gautschi, H.W.; Hofer, E.; Huber, N.E.; Schnabl, E.; Baumruker, T.
Eur. J. Immunol. 21, 377-383, 1991
A;Title: A new superfamily of lymphoid and melanoma cell proteins with extensive homo
A;Reference number: S16156; MUID:91153380; PMID:1842498
A;Accession: S16156
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-267 <GAU>
A;Cross-references: UNIPARC:UPI0001273AE; EMBL:X53795; NID:935832; PIDN:CAA37804.1; I
A;Note: the authors translated the codon AGC for residue 50 as Thr
R;Imai, T.; Fukudome, K.; Takagi, S.; Nagira, M.; Furuse, M.; Fukuhara, N.; Nishimura, J.
J. Immunol. 149, 2879-2886, 1992
A;Title: C33 antigen recognized by monoclonal antibodies inhibitory to human T cell le
D9, CD37, CD53, and CD63.
A;Reference number: A46493; MUID:93017900; PMID:1401919
A;Accession: A46493
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-239,'MV',242-267 <IMA>
A;Cross-references: UNIPARC:UPI000016B3A0; GB:S48196; NID:9258294; PIDN:AAB23825.1; P
A;Experimental source: T-cell line MOLT-4
A;Note: sequence extracted from NCBI backbone (NCBIP:117149)
C;Genetics:
A;Gene: GDB:KAI1
A;Cross-references: GDB:134216; OMIM:600623
A;Map position: 11p11.2-11p11.2
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;1-10/Domain: intracellular #status predicted <CY1>
F;11-36/Domain: transmembrane #status predicted <TM1>
F;37-57/Domain: extracellular #status predicted <EX1>
F;58-78/Domain: transmembrane #status predicted <TM2>
F;79-83/Domain: intracellular #status predicted <CY2>
F;84-108/Domain: transmembrane #status predicted <TM3>
F;109-227/Domain: extracellular #status predicted <EX2>
F;228-252/Domain: transmembrane #status predicted <TM4>
F;253-265/Domain: intracellular #status predicted <CY3>
F;129,157,198/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
Pred. No.: 1.57e-18 Length: 267
Score: 283.00 Matches: 78
Percent Similarity: 43.8% Conservative: 41
Best Local Similarity: 28.7% Mismatches: 119
Query Match: 19.8% Indels: 34
DB: 1 Gaps: 7

US-10-608-388A-1 (1-759) x A46493 (1-267)

| | | | |
|----|-----|---|-----|
| Qy | 1 | ATGGGCCAGTGGCGCATACCTCTCTCCAAAGACCGTGGTCTTTCTCAACCTCACTATCTTC | 60 |
| Db | 1 | MetGlySerAlaCysIleIysValThrIstYrPheLeuPheAsnLeuIlePhe | 20 |
| Qy | 61 | TGGGGGGCAGCTGGCATTTTATGCTATGTGGGAGCCTATGCTTCATCACTTATGATGAC | 120 |
| Db | 21 | PheIleLeuGlyAlaValIleLeuGlyPheGlyValTrpIleLeuAla | 37 |
| Qy | 121 | TATGACCATTCTTTGAAGAGATGTACAG- | 165 |
| Db | 38 | LysSerSerPheIleSerValLeuGlnThrSerSerSerLeuArgMetGlyAlaTrp | 57 |
| Qy | 166 | GTGATCATAGCTGTAGGAGCCCTGCTTTTCATCTATGGCTAATTTGGCTGCTGCCACA | 225 |
| Db | 58 | ValPheIleGlyValIleGlyAlaValThrMetLeuMetGlyPheLeuGlyCysIleGlyAla | 77 |
| Qy | 226 | ATCCGGGAAAGTCGTGGACTTCCACGTTTGTTCATCATCTGCTCTGTGTTTTTGTGC | 285 |
| Db | 78 | ValAsnGluValArgCysLeuLeuGlyLeuTyrPheAlaPheLeuLeuLeuIleLeuIle | 97 |
| Qy | 286 | ACAGAAGTTGTTAGTGGTTTTTGGGATATGTTTACAGAGCAAGGTGGAAATAGAGTT | 345 |
| Db | 98 | AlaGlnValThrAlaGlyAlaLeuPheTyrPheAsnMetGlyLysLeuLysGlnGluMet | 117 |
| Qy | 346 | GATCGCAGCATTCAGAAAGTGTATAGACCTACAATGGNACCAACCCCTGATGCTGCTAGC | 405 |
| Db | 118 | GlyGlyIleValThrGluLeuIleArgAspTyrAsnSerSerArgGluAspSerLeuGln | 137 |
| Qy | 406 | CGGGCTATTGATTATGTACAGACAGACGTGCATTGTTGTGGAAATTCACAACACTACTCAGAC | 465 |
| Db | 138 | AspAlaTrpAspTyrValGlnAlaGlnValLysCysGlyTrpValSerPheTyrAsn | 157 |
| Qy | 466 | TGGGAAATACAGATTGGTTCAAAGAAACCAAAACCAGAGTGTCCCTCTTAGTGC | 522 |
| Db | 158 | TrpThrAspAsnAlaGluLeuMetAsnArgProGluValThrTyrProCysSerCysGlu | 177 |
| Qy | 523 | -----TGCAGACAGACTGCC | 537 |
| Db | 178 | ValLysGlyGluGluAspAsnSerLeuSerValArgLysGlyPheCys---GluAlaPro | 196 |
| Qy | 538 | AGCAATTGTAATGGCAGCTGCCGCCACCTCCGAC-----CTCATGCTCAGGGGTG | 591 |
| Db | 197 | GlyAsnArgThrGlnSerGlyAsnHisProGluAspTrpProValTyrGlnGluGlyCys | 216 |
| Qy | 592 | GAGGCTCTAGTAGTGAAGAGCTACAGAAATCATGATGCATGTGATCTGGGCCCGCAGTG | 651 |
| Db | 217 | MetGluLysValGlnAlaTrpLeuGlnGluAsnLeuGlyIleLeuGlyValGlyVal | 236 |
| Qy | 652 | GCATTTGTCAGCTATTTCAGCTGCTGGGCATGCTGTGCTTGATCGTGTGTGTCAGAAGG | 711 |
| Db | 237 | GlyValAlaIleIleGluLeuLeuGlyMetValLeuSer---IleCysLeuCysArgHis | 255 |
| Qy | 712 | -----AGTAGAGATCCTGCTTAC | 729 |
| Db | 256 | ValHisSerGluAspTyrSerIysValProLysTyr | 267 |

RESULT 11
A37243
hemopoietic cell surface glycoprotein CD53 - human
N:Alternate names: pan-leukocyte surface antigen CD53
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C:Accession: A37243; A45872
R:Amiot, M.
J. Immunol. 145, 4322-4325, 1990
A:Title: Identification and analysis of cDNA clones encoding CD53. A pan-leukocyte antigen
A:Reference number: A37243; MUID:91079522; PMID:2258620
A:Accession: A37243
A:Molecule type: mRNA
A:Residues: 1-219 <AMI>
A:Cross-references: UNIPROT:P19397; UNIPARC:UPI0000000991; GB:M60871; NID:g180140; PIDN:
R:Angelisova, P.; Vleck, C.; Stefanova, I.; Lipoldova, M.; Horejsi, V.
Immunogenetics 32, 281-285, 1990

A:Title: The human leucocyte surface antigen CD53 is a protein structurally similar to

A:Reference number: A45872; MUID:91055810; PMID:1700763

A:Accession: A45872

A:Molecule type: mRNA

A:Residues: 1-219 <ANG>

A:Cross-references: UNIPARC:UPI000000D991; GB:M37033; NID:G180142; PIDN:AAA35663.1; PIFI

C:Genetics:

A:Gene: GDB:CD53; M0X44

A:Cross-references: GDB:I127521; OMIM:151525

A:Map position: 1p21-1p13.3

C:Superfamily: CD9 antigen

C:Keywords: Glycoprotein; transmembrane protein

F:1-10/Domain: intracellular #status predicted <CY1>

F:11-36/Domain: transmembrane #status predicted <TM1>

F:37-54/Domain: extracellular #status predicted <EX1>

F:55-75/Domain: transmembrane #status predicted <TM2>

F:76-80/Domain: intracellular #status predicted <CY2>

F:81-106/Domain: transmembrane #status predicted <TM3>

F:107-181/Domain: extracellular #status predicted <EX2>

F:182-204/Domain: transmembrane #status predicted <CY3>

F:205-219/Domain: intracellular #status predicted <CY4>

F:123,148/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 1-25e-17 | Length: | 219 |
| Score: | 273.50 | Matches: | 65 |
| Percent Similarity: | 46.2% | Conservative: | 44 |
| Best Local Similarity: | 27.5% | Mismatches: | 100 |
| Query Match: | 19.1% | Indels: | 27 |
| DB: | 1 | Gaps: | 4 |

US-10-608-388A-1 (1-759) x A37243 (1-219)


```
QY 601 GTAGTGAAGAAGCTACAGAATAATCATGATGATGTGATCTGGCGGCACTGGCATTTGCA 660
Db 174 AlaArgLeuTrpPheHisSerAsnPheLeuTyrileGlylleIleThrIleCysValCys 193
QY 661 GCTATTACGCTGGGGCATGCTGTGCTTGGCATCGGTGGTGAGCA 708
Db 194 VallileGluValLeuGlyMetSerPheAlaLeuThrLeuAsnCysGln 209

RESULT 12
A59262
tetraspan TSPAN-1 - human
C;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: A59262
R;Todd, S.C.; Doctor, V.S.; Levy, S.
Biochim. Biophys. Acta 1399, 101-104, 1998
A;Title: Sequences and expression of six new members of the tetraspanin/TM4SP family.
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-241 <TOD>
A;Cross-references: UNIPROT:O60635; UNIPARC:UPI0000004BE36; GB:AF054838; NID:g2997740; PI
C;Genetics:
A;Gene: TSPAN-1
C;Superfamily: CD9 antigen

Alignment Scores:
Pred. No.: 1.23e-16 Length: 241
Score: 263.00 Matches: 68
Percent Similarity: 46.5% Conservative: 45
Best Local Similarity: 28.0% Mismatches: 114
Query Match: 18.4% Indels: 16
DB: 2 Gaps: 6

US-10-608-388A-1 (1-759) x A59262 (1-241)
QY 7 CAGTGGCGGCATCCTCTCCAGACGCTGCTGCTTTCTCAACCTCATCTTCTGGGG 66
Db 2 GlnCys---PheSerPheIleLysThrMetMetIleLeuPheAsnLeuLeuIlePheLeu 20
QY 67 GCAGCTGGCATTTTATGCTATGTGGGAGCCTATGCTTTCATCTTATGATGACTATGAC 126
Db 21 CysGlyAlaAlaLeuLeuAlaValGlyIleTrpValSerIleAspGlyAlaSerPheLeu 40
QY 127 CACTTCTTGAAGATGTACACGCTCATCCCTGCTAGTG-----ATC 171
Db 41 LysIlePheGlyProLeuSerSerSerAlaMetGlnPheValAsnValGlyTyrPheLeu 60
QY 172 ATAGCTGTAGAGCCCTGCTTTTCATCATTTGGGCTAATTGGCTGCTGTGCCACAAATCCGG 231
Db 61 IleAlaAlaGlyValValValPheAlaLeuGlyPheLeuGlyCysTyrGlyAlaLysThr 80
QY 232 GAAAGTCGCTGTGGACTTGGCAGCTTTGTATCATCATCTGCTTGTGTTTTGTACAGAA 291
Db 81 GluSerLysCysAlaLeuValThrPhePhePheIleLeuLeuLeuIlePheIleAlaGlu 100
QY 292 GTTGTGTAGTGGTTTGGGATATGTTTACAGACCAAGGTGGAATAGGTGATCGC 351
Db 101 ValAlaAlaAlaValValAlaLeuValTyrThrThrMetAlaGluHisPheLeuThrLeu 120
QY 352 AGCATTCAGAAAGGTATACACCTACAAATGGACCAACCTCATGCTGTAGCCGGCT 411
Db 121 LeuValValProAlaIleLysLysAspTyrGlySerGlnGluAsp----PheThrGlnVal 139
QY 412 ATTGATTATACAGACAGCTGCATTTGTTGGAAATTCACAACTACTCAGACTGGAA 471
Db 140 TrpAsnThrThrMetLysGlyLeuLysCysGlyPheThrAsnTyrThrAspPheGlu 159
QY 472 AATACAGATTGGTTTCAAGAAACCAAAACACAGAGTCCCTCTTACCTGTCAGAGAG 531
Db 160 AspSerProTyrPheLysGlu-----AsnSerAlaPheProPheCysCysAsnAsp 177
```

```
QY 532 ACTGCCAGCAAT-----TGTATATGGCAGCTGGCCACCTTCGACCTC 576
Db 178 AsnValThrAsnThrAlaAsnGluThrCysThrGluGlnLysAlaHis-----AspGln 195
QY 577 TATGCTGAGGGGTGTGAGGCTCTAGTAGTGAAGAAGCTACAAGAAATCATGATCATGTG 636
Db 196 LysValGluGlyCysPheAsnGlnLeuLeuTyrAspIleArgThrAsnAlaValThrVal 215
QY 637 ATCTGGGCGCACTGGCATTTGCGAGCTATTACGCTGCTGGCAGCTGTGCTTGCATC 696
Db 216 GlyGlyValAlaAlaGlyIleGlyGlyLeuGluLeuAlaAlaMetIleValSerMetTyr 235
QY 697 GTGTTGTGC 705
Db 236 LeuTyrCys 238

RESULT 13
A39574
leukocyte antigen OX-44 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Aug-1991 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C;Accession: A39574
R;Bellacosa, A.; Izzo, P.A.; Bear, S.E.; Tsichlis, P.N.
Mol. Cell. Biol. 11, 2864-2872, 1991
A;Title: The rat leukocyte antigen MRC OX-44 is a member of a new family of cell surf:
A;Reference number: A39574; MUID:91203909; PMID:2017181
A;Accession: A39574
A;Molecule type: mRNA
A;Residues: 1-219 <BEL>
A;Cross-references: UNIPROT:P24485; UNIPARC:UPI000004F1F0; GB:M57276; NID:g205897; PII
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;1-10/Domain: intracellular #status predicted <EX1>
F;11-36/Domain: transmembrane #status predicted <TM1>
F;37-54/Domain: extracellular #status predicted <EX2>
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F;205-219/Domain: intracellular #status predicted <CY3>
F;119,129,148/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Pred. No.: 2.64e-16 Length: 219
Score: 259.50 Matches: 61
Percent Similarity: 45.3% Conservative: 46
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DB: 1 Gaps: 4

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US-10-608-388A-1 (1-759) x B47629 (1-281)

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| Qy | 88 | GTGGGAGCCTATGCTCTTCATCACTTATGACATGACCTCTCTTTGAAGATGTGTAC | 147 |
| Db | 32 | PheGlyThrTrpIleLeuIleAspLysThrSerPheValSerPheValGly | 49 |
| Qy | 148 | ACGCTCATCCCT-----GCTGTAGTATCATAGCTGTAGGAGCCCTGCTTTTC | 195 |
| Db | 50 | SerPheValProLeuGlnThrTrpSerLysValLeuSerValSerGlyValLeuThrMet | 69 |
| Qy | 196 | ATCATTGGGCTAATTGGTGTGCTGCCACAATCCGGGAAAGTCCGTCTGGACCTTGCACG | 255 |
| Db | 70 | AlaLeuAlaLeuGlyCysValGlyAlaLeuLysGluLeuArgCysLeuLeuGlyLeu | 89 |
| Qy | 256 | TTTGTTCATCATCTCTCTGCTGTTTGTCTACAGAAGTTGTTAGTGGTGTGGGATAT | 315 |
| Db | 90 | TyrPheGlyMetLeuLeuLeuPheAlaThrGlnIleThrLeuGlyIleLeuIleSer | 109 |
| Qy | 316 | GTTTTCAGAGCAAAAGTGAAATGAGGTGATCGCAGCATTCAGAAAGTGATAAGACC | 375 |
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| Qy | 376 | TACAATGGAAACCAACCTCGAT-----GCTCTAGCCGGCTATTGATATTGTACACAGA | 429 |
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| Qy | 430 | CAGCTGCATTTGTTGGAAATTCACAACCTACTCAGACTGGGAAATACAGATTGGTTCAA | 489 |
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| Qy | 490 | GAACCAAAAACACAGT-----GTCCTCTTAGCTGCTGCAGAGAGACTGCCACCAT | 543 |
| Db | 169 | AlaAsnGlySerGluGluLeuPheValProCysSerCysTrpAsnSerThrAlaThrAsn | 188 |
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| Qy | 553 | -----AGCTGGCCCCCTTCCGACCTCTATGCTGAG | 585 |
| Db | 209 | LysLeuArgGlnThrAlaAspIleCysAlaLeuProAlaLysAlaHisIleTyrArgGlu | 228 |
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| Db | 229 | GlyCysAlaArgSerLeuGlnLysTrpLeuHisAsnAsnIleIleSerIleValGlyIle | 248 |
| Qy | 646 | GCATCTGGCATTTGCAAGCTATTACAGCTGTGGGCAATGCTGTGCTGCTCATCTGTTGTC | 705 |
| Db | 249 | CysLeuGlyValGlyLeuLeuGlu---LeuGlyPheMetThrLeuSerIlePheLeuCys | 267 |
| Qy | 706 | AGAAGAGTAGAGATCTGCTTACAGAGCTCCTC | 738 |
| Db | 268 | ---ArgAsnLeuAspHisValTyrAspArgLeu | 277 |

Search completed: April 4, 2006, 21:33:03
Job time : 46.5 secs

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 4, 2006, 21:34:40 ; Search time 11.3 Seconds
(without alignments)
1819.174 Million cell updates/sec

Title: US-10-608-388A-1

Perfect score: 1429

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Searched: 572472 seqs, 135419439 residues

Total number of hits satisfying chosen parameters: 1144944

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SID55/ptodata/2/paa/US06 NEW COMB.pep.*
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8: /SID55/ptodata/2/paa/US60 NEW COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1336 | 93.5 | 253 | 6 | US-10-917-503B-11412 |
| 3 | 1329 | 93.0 | 253 | 6 | US-10-917-503B-11363 |
| 4 | 143.5 | 24.0 | 244 | 6 | US-10-529-348-2235 |
| 5 | 332 | 23.2 | 253 | 6 | US-11-268-554-266 |
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| 7 | 332 | 23.2 | 253 | 6 | US-11-268-554-269 |
| 8 | 332 | 23.2 | 253 | 6 | US-11-268-554-272 |
| 9 | 332 | 23.2 | 253 | 6 | US-10-567-867-1300 |

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| 10 | 332 | 23.2 | 253 | 7 | US-11-385-692-2034 | Sequence 2034, Ap |
| 11 | 332 | 23.2 | 253 | 7 | US-11-385-692-2035 | Sequence 2035, Ap |
| 12 | 332 | 23.2 | 253 | 7 | US-11-385-692-2037 | Sequence 2037, Ap |
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| 14 | 331 | 23.2 | 253 | 6 | US-11-268-554-273 | Sequence 273, App |
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| 20 | 304 | 21.3 | 211 | 7 | US-11-385-692-2036 | Sequence 2036, App |
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| 25 | 297.5 | 20.8 | 238 | 6 | US-11-332-890-2 | Sequence 2, Appli |
| 26 | 297.5 | 20.8 | 238 | 8 | US-60-741-048-216 | Sequence 216, App |
| 27 | 297.5 | 20.8 | 238 | 8 | US-60-741-048-217 | Sequence 217, App |
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| 31 | 283 | 19.8 | 267 | 8 | US-60-763-374-1 | Sequence 1, Appli |
| 32 | 282.5 | 19.8 | 239 | 6 | US-10-917-503B-13815 | Sequence 13815, A |
| 33 | 282.5 | 19.8 | 239 | 6 | US-10-567-867-1603 | Sequence 1603, Ap |
| 34 | 282.5 | 19.8 | 239 | 8 | US-60-751-420-2526 | Sequence 2526, Ap |
| 35 | 282 | 19.7 | 267 | 8 | US-60-763-374-3 | Sequence 3, Appli |
| 36 | 282 | 19.7 | 267 | 8 | US-60-763-374-4 | Sequence 4, Appli |
| 37 | 282 | 19.7 | 331 | 8 | US-60-763-374-2 | Sequence 2, Appli |
| 38 | 273.5 | 19.1 | 219 | 5 | US-09-836-544D-36 | Sequence 36, Appl |
| 39 | 263 | 18.4 | 241 | 6 | US-11-191-274A-76 | Sequence 76, Appl |
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| 41 | 263 | 18.4 | 241 | 6 | US-11-191-274A-78 | Sequence 78, Appl |
| 42 | 263 | 18.4 | 241 | 6 | US-11-191-274A-79 | Sequence 79, Appl |
| 43 | 263 | 18.4 | 241 | 6 | US-11-191-274A-80 | Sequence 80, Appl |
| 44 | 263 | 18.4 | 241 | 6 | US-11-191-274A-81 | Sequence 81, Appl |
| 45 | 263 | 18.4 | 241 | 6 | US-11-344-932-114 | Sequence 114, App |

ALIGNMENTS

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; Sequence 11371, Application US/10917503B
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HAYASHI, KOJI
; APPLICANT: SAITO, KAORI
; APPLICANT: YAMAMOTO, JUNICHI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: WAKAMATSU, AI
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: OTSUKI, TETSUJI
; TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH CDNA AND THEIR USE
; FILE REFERENCE: 084335/0123
; CURRENT APPLICATION NUMBER: US/10/917,503B
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US/09/629,469
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: JP 1999-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 1999-300253
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/159,590
; PRIOR FILING DATE: 1999-10-18

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; PRIOR APPLICATION NUMBER: 60/183,322
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 19025
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11371
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-503B-11371

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Query Match: 93.5% Indels: 0
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; APPLICANT: OYA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HAYASHI, KOJI
; APPLICANT: SAITO, KAORU
; APPLICANT: YAMAMOTO, JUNICHI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: WAKAMATSU, AI
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: OTSUKI, TETSUJI
; TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH cDNA AND THEIR USE
; FILE REFERENCE: 084335/0123
; CURRENT APPLICATION NUMBER: US/10/917,503B
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US/09/629,469
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: JP 1999-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 1999-300253
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183,322
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 19025
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11412
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-503B-11412

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Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
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Qy 241 TGTGACTTGCACGTTTGTCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
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; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HAYASHI, KOJI
; APPLICANT: SAITO, KAORU
; APPLICANT: YAMAMOTO, JUNICHI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: WAKAMATSU, AI
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: OTSUKI, TETSUJI
; TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH cDNA AND THEIR USE
; FILE REFERENCE: 084335/0123
; CURRENT APPLICATION NUMBER: US/10/917,503B
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US/05/629,469
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: JP 1999-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 1999-300253
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183,322
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 19025
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11363
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-503B-11363
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Best Local Similarity: 99.6% Mismatches: 1
Query Match: 93.0% Indels: 0
DB: Gaps: 0
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US-10-608-388A-1 (1-759) x US-10-917-503B-11363 (1-253)

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Qy 1 ATGGGCGAGTGGCGCATACCTCTCTCAAGACCGTGTCTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
Qy 61 TGGGGGCGAGCTGGCGATTTTATGCTATGCTGGGAGCTATGCTTCTCATCTTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
Qy 121 TATGACCACTTCTTTTGAAGATGTGTACAGCTCATCCCTGCTGTAGTGATCATAGCTGTA 180
Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleIleAlaVal 60
Qy 181 GGAGCCCTGCTTTTTCATCATTTGGGCTAATTGGCTGTGTGCCACAATCCGGGAAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
Qy 241 TGTGGAGTTGCCACAGCTTTCATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuLeuValPheValThrGluValAlaVal 100
Qy 301 GTGGTTTGGGATATGTTTACAGAGCAAAAGTGGAAATGAGTGTGATCGCAGCATTCAG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
Qy 361 AAAGTGTATAGACCTCAATGGAACCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaLaserArgAlaIleAspTyr 140
Qy 421 GTACAGACAGCTGCGCTATTGTTGTGAATTCACAACTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTyrGluAsnThrAsp 160
Qy 481 TGGTTCAAAGAAACCAAAACCAAGAGAGTGTCCCTTCTAGCTGCTGCAGAGAGCTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
Qy 541 AATTGTAATGGCAGCTGGCCACCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
Qy 601 GTAGTGAAGAGCTACAAAGAAATCATGATGATGATCTGGCCGCACTGGCATTTGCA 660
Db 201 ValValLysLysLeuGlnGluMetMetHisValIleTrpAlaLeuAlaPheAla 220
Qy 661 GCTATTGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysGlyArgSerArgAsp 240
Qy 721 CCTGCTTACGAGCTCCTCATCACTGGCGGAACCTATGCA 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253
```

RESULT 4

```
US-10-529-348-2235
; Sequence 2235, Application US/10529348
; GENERAL INFORMATION:
; APPLICANT: Bodary-Winter, Sarah
; APPLICANT: Clark, Hilary
; APPLICANT: Jackman, Janet
; APPLICANT: Schoenfeld, Jill
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
```

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; APPLICANT: Wu,Thomas D.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR THE TREATMENT OF PSORIASIS
; FILE REFERENCE: P1987R1-US
; CURRENT APPLICATION NUMBER: US/10/529,348
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/030907
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 60/414,006
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 2484
; SEQ ID NO 2235
; LENGTH: 244
; TYPE: prt
; ORGANISM: Homo sapien
US-10-529-348-2235

```

| | | | |
|------------------------|----------|---------------|-----|
| Alignment Scores: | 3.07e-25 | Length: | 244 |
| Pred. No.: | 343.50 | Matches: | 85 |
| Score: | 50.2% | Conservative: | 41 |
| Percent Similarity: | 3.9% | Mismatches: | 102 |
| Best Local Similarity: | 23.0% | Indels: | 23 |
| Query Match: | 6 | Gaps: | 7 |
| DB: | | | |

US-10-608-388A-1 (1-759) x US-10-529-348-2235 (1-244)

[illegible]

```

Qy      706 AGAGGAGTAGAGATCCTGCTTACGAGTCCTC 738
       |||
Db      234 ArgPheIleThrAlaasnGlnTrpGluMetVal 244
       |||||
RESULT 5
US-11-268-554-266
; Sequence 266, Application US/11268554
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno et al.
; TITLE OF INVENTION: PANCREATIC CANCER TARGETS AND
; TITLE OF INVENTION: THEROF
; FILE REFERENCE: CL001557
; CURRENT APPLICATION NUMBER: US/11/268,554
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 1004
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 266
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-268-554-266

```

| | | |
|------------------------|-----------|---------------|
| Alignment Scores: | | |
| Pred. No.: | 4, 21e-24 | Length: |
| Score: | 332.00 | Matches: |
| Percent Similarity: | 51.1% | Conservative: |
| Best Local Similarity: | 28.8% | Mismatches: |
| Query Match: | 23.2% | Indels: |
| DB: | 6 | Gaps: |
| | | 253 |

US-10-608-388A-1 (1-759) x US-11-268-554-266 (1-253)

| | | | | |
|----|-----|--|---------------------------------------|----|
| Qy | 10 | TGGGGCATCCTCTCTCCAGA | CGGTGCTGTCTTTCTCAACCTCATCTTCTGGGGGGCA | 69 |
| Db | 11 | CysgylThrValCysLeuLysLeuLeuPheThrYrAsnCysCysPheTrpLeuAla | 30 | |
| Qy | 70 | GCTGGCATTTATGCTATGTGGGAGCTATGTCTTCATCACTTATGATGACTATGACCAC | 129 | |
| Db | 31 | GlyLeuAlaValMetAlaValGlyIleThrPrhLeuAlaLeuLysSerAspYrIleSer | 50 | |
| Qy | 130 | TTCTTTGAAGATGTGACAGCTCATCCCTGCTGTAGTGATCATAGCTGTAGGAGCCCTG | 189 | |
| Db | 51 | LeuLeuAlaSerGlyThrYrLeuAlaThrAlaYrIleLeuValAlaIalaglyThrVal | 70 | |
| Qy | 190 | CTTTTCATCATGGCTAAATGGCTGTGTGCCCAATCCGGGAAAGTCGTGTGGACTT | 249 | |
| Db | 71 | ValMetValThrGlyValLeuGlyCysCysAlaThrPheLysGluArgAsnLeuLeu | 90 | |
| Qy | 250 | GCACGTTTGTATCATCTCTGCTCTTGGTTTCTTCACAGAAAGTTGTTGACTGTTTGT | 309 | |
| Db | 91 | ArgLeuYrPheIleLeuLeuLeuIlePheLeuLeuGluIleIleIalaglyIleu | 110 | |
| Qy | 310 | GGATATCTTTACAGACGAAAGGTCGAAAATGAGGTTGATCGACGATTTCAG--- | 366 | |
| Db | 111 | AlaYrAlaYrYrGlnGlnLeuAsnThrGluLeuLysGluAsnLeuLysAspThrMet | 130 | |
| Qy | 367 | TATAAGACCTACAATGGAAACCAACCTGTATGCTGTACCGGGCTATTGATTATGTACAG | 426 | |
| Db | 131 | ThrLysArgYrHisGlnProGlyHisGluAlaValThrSerAlaValAspGlnLeuGln | 150 | |
| Qy | 427 | AGACAGCTGATGTTCTGTGGAAATTCACAACTACTCAGACTCGSAAATACAGATTGGTTC | 486 | |
| Db | 151 | GlnGluPheHisCysCysGlySerAsnAsnSerGlnAspTrpArgAspSerGluTrpIle | 170 | |
| Qy | 487 | AAA-----GAAACCAAAACACAGATGTCCCTCTTAGCTGTGCAGAGACTGCCAGC | 540 | |
| Db | 171 | ArgSerGlnGluAlaGlyArgValValProAspSerCysLysThrValValAla | 190 | |
| Qy | 541 | AATTGTAATGGCAGCTGGGCCACCTTCGACCTCTAT-----GCTGAGGGGTGTGAG | 594 | |
| Db | 191 | LeuCys---GlnGlnArgAspHisAlaSerAsnIleYrLysValGluGlyCysIle | 209 | |


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Db 171 ArgSerGlnGluAlaGlyGlyArgValValProAspSerCysCysLysThrValValAla 190
Qy 541 AATTGTAATGGCAGCTGGCCACCTTCCGACCTCTAT-----GCTGAGGGGTGTGAG 594
Db 191 LeuCys---GlyGlnArgAspHisAlaSerAsnIleTyrLysValGluGlyGlyCysIle 209
Qy 595 GCTCTAGTAGTGAAGAAGCTACAAGAAATCATGATGTCATGTGCTGGCCGCGCACTGGCA 654
Db 210 ThrLysLeuGluThrPheIleGlnGluHisLeuArgValIleGlyAlaValGlyIleGly 229
Qy 655 TTTCGACGATTTCAGCTCTGGGCGCATGCTGTGTCTTCC 693
Db 230 IleAlaCysValGlnValPheGlyMetIlePheThrCys 242

RESULT 8
US-11-268-554-272
; Sequence 272, Application US/11268554
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno et al.
; TITLE OF INVENTION: PANCREATIC CANCER TARGETS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01557
; CURRENT APPLICATION NUMBER: US/11/268,554
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 1004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 272
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-268-554-272

Alignment Scores:
Pred. No.: 4,21e-24 Length: 253
Score: 332.00 Matches: 67
Percent Similarity: 51.1% Conservative: 52
Best Local Similarity: 28.8% Mismatches: 108
Query Match: 23.2% Indels: 6
DB: Gaps: 4

US-10-608-388a-1 (1-759) x US-11-268-554-272 (1-253)
Qy 10 TGGCGCATCACCTCTCCAGACCGTCTGTGTTCTTCTCAACCTCATCTTCTGGGGGCA 69
Db 11 CysGlyThrValCysLeuLysTyrLeuLeuPheThrTyrAsnCysCysPheTrpLeuAla 30
Qy 70 GCTGCGCATTTTATGCTATGTGGAGCCTATGCTTCATCATCACTATGATGACTATGACCAC 129
Db 31 GlyLeuAlaValMetAlaValGlyIleTrpThrLeuAlaLeuLysSerAspTyrIleSer 50
Qy 130 TTCTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTGTATGATCATAGTGTAGGACCCCTG 189
Db 51 LeuLeuAlaSerGlyThrTyrLeuAlaThrAlaTyrIleLeuValValAlaGlyThrVal 70
Qy 190 CTTTTCATCATTTGGCTAATTCGGCTGTGTCACCAATCCGGGAAAGTCGCTGTGGACTT 249
Db 71 ValMetValThrGlyValLeuGlyCysCysAlaThrPheLysGluArgAsnLeuLeu 90
Qy 250 GCCAGCTTTGTCATCTCTCTGTTGTTTGTTCACAGAGTTGTTGTAGTGTGTTTGT 309
Db 91 ArgLeuTyrPheIleLeuLeuIlePheLeuLeuGluIleAlaGlyIleLeu 110
Qy 310 GGATATGTTTACAGACGAAGGTGGAATATGAGTTGATTCGACGATTCAG---AAAGTG 366
Db 111 AlaTyrAlaTyrTyrGlnGlnLeuAsnThrGluLeuLysGluAsnLeuLysAspThrMet 130
Qy 367 TATAGACTACAAAGGAACCAACCTGATGCTGTAGCGGGCTATTGATATGATACAG 426
Db 131 ThrLysArgTyrHisGlnProGlyHisGluAlaValThrSerAlaValAspGlnLeuGln 150
Qy 427 AGACAGCTGCATTGTTGTGGAAATTCACAACTACTCAGACTCTGGAATAATACAGATTGTTTC 486
Db 151 GlnGluPheHisCysCysGlySerAsnAsnSerGlnAspTyrArgAspSerGluTrpIle 170

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Qy 487 AAA-----GAACCAAAACCAGAGTGTCCCTCTTAGCTGCTGCAGAGAGACTGCCAGC 540
Db 171 ArgSerGlnGluAlaGlyGlyArgValValProAspSerCysCysLysThrValValAla 190
Qy 541 AATTGTAATGGCAGCTGGCCACCTTCCGACCTCTAT-----GCTGAGGGGTGTGAG 594
Db 191 LeuCys---GlyGlnArgAspHisAlaSerAsnIleTyrLysValGluGlyGlyCysIle 209
Qy 595 GCTCTAGTAGTGAAGAAGCTACAAGAAATCATGATGTCATGTGCTGGCCGCGCACTGGCA 654
Db 210 ThrLysLeuGluThrPheIleGlnGluHisLeuArgValIleGlyAlaValGlyIleGly 229
Qy 655 TTTCGACGATTTCAGCTCTGGGCGCATGCTGTGTCTTCC 693
Db 230 IleAlaCysValGlnValPheGlyMetIlePheThrCys 242

RESULT 9
US-10-567-867-1300
; Sequence 1300, Application US/10567867
; GENERAL INFORMATION:
; APPLICANT: Li, Martha
; APPLICANT: Rupnow, Brent A.
; APPLICANT: Webster, Kevin R.
; APPLICANT: Jackson, Donald
; APPLICANT: Wong, Tai W.
; TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
; FILE REFERENCE: D0310 PCT
; CURRENT APPLICATION NUMBER: US/10/567,867
; CURRENT FILING DATE: 2006-01-27
; PRIOR APPLICATION NUMBER: US 60/490,890
; PRIOR FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 2786
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1300
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-567-867-1300

Alignment Scores:
Pred. No.: 4,21e-24 Length: 253
Score: 332.00 Matches: 67
Percent Similarity: 51.1% Conservative: 52
Best Local Similarity: 28.8% Mismatches: 108
Query Match: 23.2% Indels: 6
DB: Gaps: 4

US-10-608-388a-1 (1-759) x US-10-567-867-1300 (1-253)
Qy 10 TGGCGCATCACCTCTCCAGACCGTCTGTGTTCTTCTCAACCTCATCTTCTGGGGGCA 69
Db 11 CysGlyThrValCysLeuLysTyrLeuLeuPheThrTyrAsnCysCysPheTrpLeuAla 30
Qy 70 GCTGCGCATTTTATGCTATGTGGAGCCTATGCTTCATCATCACTATGATGACTATGACCAC 129
Db 31 GlyLeuAlaValMetAlaValGlyIleTrpThrLeuAlaLeuLysSerAspTyrIleSer 50
Qy 130 TTCTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTGTATGATCATAGTGTAGGACCCCTG 189
Db 51 LeuLeuAlaSerGlyThrTyrLeuAlaThrAlaTyrIleLeuValValAlaGlyThrVal 70
Qy 190 CTTTTCATCATTTGGCTAATTCGGCTGTGTCACCAATCCGGGAAAGTCGCTGTGGACTT 249
Db 71 ValMetValThrGlyValLeuGlyCysCysAlaThrPheLysGluArgAsnLeuLeu 90
Qy 250 GCCAGCTTTGTCATCTCTCTGTTGTTTGTTCACAGAGTTGTTGTAGTGTGTTTGT 309
Db 91 ArgLeuTyrPheIleLeuLeuIlePheLeuLeuGluIleAlaGlyIleLeu 110
Qy 310 GGATATGTTTACAGACGAAGGTGGAATATGAGTTGATTCGACGATTCAG---AAAGTG 366
Db 111 AlaTyrAlaTyrTyrGlnGlnLeuAsnThrGluLeuLysGluAsnLeuLysAspThrMet 130

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QY 367 TATAAGACCTACAATGGAACCAACCTGCTGCTAGCCGGCTATTGATTGTACAG 426
Db 131 ThrLysArgTyrHisGlnProGlyHisGluAlaValThrSerAlaValAspGlnLeuGln 150
QY 427 AGACAGCTGCTATTGTTGGAAATTCACAACTACTCAGACTGGGAAATACAGATTGGTTC 486
Db 151 GlnGluPheHisCysCysGlySerAsnAsnSerGlnAspTrpArgAspSerGluTrpIle 170
QY 487 AAA-----GAAACCAAAACCAAGAGTGCCTCTTACGACTCTAT-----GCTGAGGGGTGTGAG 540
Db 171 ArgSerGlnGluAlaGlyArgValProAspSerCysCysLysThrValValAla 190
QY 541 AATTGTAATGCGACCTGGCCACCCTTCGACCTCTAT-----GCTGAGGGGTGTGAG 594
Db 191 LeuCys---GlyGlnArgAspHisAlaSerAsnIleTyrLysValGluGlyCysIle 209
QY 595 GCTCTAGTAGTGAAGAGCTACAGAAATCATGATGTCGTGCTGCTTGC 654
Db 210 ThrLysLeuGluThrPheIleGlnGluHisLeuArgValIleGlyAlaValGlyIleGly 229
QY 655 TTGCGACTATTACGCTGGGCGATGCTGTGCTTGC 693
Db 230 IleAlaCysValGlnValPheGlyMetIlePheThrCys 242

RESULT 10
US-11-385-692-2034
; Sequence 2034, Application US/11385692
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: KIDNEY DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL0015910RD
; CURRENT APPLICATION NUMBER: US/11/385,692
; CURRENT FILING DATE: 2006-03-22
; NUMBER OF SEQ ID NOS: 6044
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2034
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-385-692-2034

Alignment Scores:
Pred. No.: 4,21e-24 Length: 253
Score: 332.00 Matches: 67
Percent Similarity: 51.1% Conservative: 52
Best Local Similarity: 28.8% Mismatches: 108
Query Match: 23.2% Indels: 6
DB: 7 Gaps: 4

US-10-608-388A-1 (1-759) x US-11-385-692-2034 (1-253)
QY 10 TGGGGCATCACCTCTCCAAAGACCGTGTGCTCTTCTCAACCTCATCTTCTGGGGGCA 69
Db 11 CysGlyThrValCysLeuLysTyrLeuLeuPheThrTyrAsnCysCysPheTrpLeuAla 30
QY 70 GCTGGCATTTTATGCTATGTTGGAGCCTATGCTTCTATCATCTATGATGATGATGACCAC 129
Db 31 GlyLeuAlaValMetAlaValGlyIleTrpThrLeuAlaLeuLysSerAspTyrIleSer 50
QY 130 TTCTTTGAAGATGTGTACAGCTCATCTCCCTGCTGTAGTGTATGATCATGCTGTAGGCGCTG 189
Db 51 LeuLeuAlaSerGlyThrTyrLeuAlaThrAlaTyrIleLeuValValAlaGlyThrVal 70
QY 190 CTTTTCATCATTTGGCTAAATGGCTGTGTCACCAATCCGGAAAGTCCGCTGTGGACTT 249
Db 71 ValMetValThrGlyValLeuGlyCysCysAlaThrPheLysGluArgAsnLeuLeu 90
QY 250 GCCACGTTTGTATCATCTCTGCTCTTGGTTTGTGTACAGAAAGTGTGTAGTGGTTTG 309
Db 91 ArgLeuTyrPheIleLeuLeuIleIlePheLeuLeuGluIleIleAlaGlyIleLeu 110
QY 310 GGATATGTTTACAGCAAGGTGGAATAAGAGTTGATCGCAGCATTCAG---AAAGTG 366
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Db 111 AlaTyrAlaTyrTyrGlnGlnLeuAsnThrGluLeuLysGluAsnLeuLysAspThrMet 130
QY 367 TATAAGACCTACAATGGAACCAACCTGCTGCTAGCCGGCTATTGATTGTACAG 426
Db 131 ThrLysArgTyrHisGlnProGlyHisGluAlaValThrSerAlaValAspGlnLeuGln 150
QY 427 AGACAGCTGCTATTGTTGGAAATTCACAACTACTCAGACTGGGAAATACAGATTGGTTC 486
Db 151 GlnGluPheHisCysCysGlySerAsnAsnSerGlnAspTrpArgAspSerGluTrpIle 170
QY 487 AAA-----GAAACCAAAACCAAGAGTGCCTCTTACGACTCTAT-----GCTGAGGGGTGTGAG 540
Db 171 ArgSerGlnGluAlaGlyArgValProAspSerCysCysLysThrValValAla 190
QY 541 AATTGTAATGCGACCTGGCCACCCTTCGACCTCTAT-----GCTGAGGGGTGTGAG 594
Db 191 LeuCys---GlyGlnArgAspHisAlaSerAsnIleTyrLysValGluGlyCysIle 209
QY 595 GCTCTAGTAGTGAAGAGCTACAGAAATCATGATGTCGTGCTGCTTGC 654
Db 210 ThrLysLeuGluThrPheIleGlnGluHisLeuArgValIleGlyAlaValGlyIleGly 229
QY 655 TTGCGACTATTACGCTGGGCGATGCTGTGCTTGC 693
Db 230 IleAlaCysValGlnValPheGlyMetIlePheThrCys 242

RESULT 11
US-11-385-692-2035
; Sequence 2035, Application US/11385692
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: KIDNEY DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL0015910RD
; CURRENT APPLICATION NUMBER: US/11/385,692
; CURRENT FILING DATE: 2006-03-22
; NUMBER OF SEQ ID NOS: 6044
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2035
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-385-692-2035

Alignment Scores:
Pred. No.: 4,21e-24 Length: 253
Score: 332.00 Matches: 67
Percent Similarity: 51.1% Conservative: 52
Best Local Similarity: 28.8% Mismatches: 108
Query Match: 23.2% Indels: 6
DB: 7 Gaps: 4

US-10-608-388A-1 (1-759) x US-11-385-692-2035 (1-253)
QY 10 TGGGGCATCACCTCTCCAAAGACCGTGTGCTCTTCTCAACCTCATCTTCTGGGGGCA 69
Db 11 CysGlyThrValCysLeuLysTyrLeuLeuPheThrTyrAsnCysCysPheTrpLeuAla 30
QY 70 GCTGGCATTTTATGCTATGTTGGAGCCTATGCTTCTATCATCTATGATGATGACCAC 129
Db 31 GlyLeuAlaValMetAlaValGlyIleTrpThrLeuAlaLeuLysSerAspTyrIleSer 50
QY 130 TTCTTTGAAGATGTGTACAGCTCATCTCCCTGCTGTAGTGTATGATCATGCTGTAGGCGCTG 189
Db 51 LeuLeuAlaSerGlyThrTyrLeuAlaThrAlaTyrIleLeuValValAlaGlyThrVal 70
QY 190 CTTTTCATCATTTGGCTAAATGGCTGTGTCACCAATCCGGAAAGTCCGCTGTGGACTT 249
Db 71 ValMetValThrGlyValLeuGlyCysCysAlaThrPheLysGluArgAsnLeuLeu 90
QY 250 GCCACGTTTGTATCATCTCTGCTCTTGGTTTGTGTACAGAAAGTGTGTAGTGGTTTG 309
Db 91 ArgLeuTyrPheIleLeuLeuIleIlePheLeuLeuGluIleIleAlaGlyIleLeu 110
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QY 310 GGATATGTTTACAGAGCAAAAGTGGAAAATGAGTTGATCGCAGCATTCAG---AAAGTG 366
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
111 AlatyAlatyTyTyGlnGlnLeuAsnThrGlnLeuLysGluAsnLeuLysAspThrMet 130
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
367 TATAAGACCTCAATAGGAACCAACCTGCTGCTAGCCGGCTATTGATTATGTATGACAG 426
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
131 ThrLysArgTyHisGlnProGlyHisGlnAlaValThrSerAlaValAspGlnLeuGln 150
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
427 AGACAGCTGCATTTGTTGGAAATTCACAACTACTCAGACTGGGAAAATACAGATTGGTTC 486
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
151 GlnGluPheHisCysCysGlySerAsnAsnSerGlnAspTrpArgAspSerGluTrpIle 170
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
487 AAA-----GAACCAAAAACAGAGTCTCCCTCTTACTGCTGCTCAGAGAGACTGCCAGC 540
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
171 ArgSerGlnGluAlaGlyGlyArgValValProAspSerCysLysValValAla 190
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
541 AATTGTAATGGCAGCTGGCCACCTCCGACCTCTAT-----GCTGAGGGGTGTGAG 594
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
191 LeuCys---GlyGlnArgAspHisAlaSerAsnIleTyLysValGluGlyCysIle 209
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
595 GCTCTAGTAGTGAAGAACTACAAGAAATCATGATGATGATCTGGCGCGCATGGCA 654
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
210 ThrLysLeuGluThrPheIleGlnHisLeuArgValIleGlyAlaValGlyIleGly 229
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
655 TTTCAGCTATTACGCTGCTGGCATGCTGTGTCTTGC 693
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
230 IleAlaCysValGlnValPheGlyMetIlePheThrCys 242

```

RESULT 12

```

US-11-385-692-2037
; Sequence 2037, Application US/11385692
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: KIDNEY DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL0015910RD
; CURRENT APPLICATION NUMBER: US/11/385,692
; CURRENT FILING DATE: 2006-03-22
; NUMBER OF SEQ ID NOS: 6044
; SOFTWARE: FastSeq for Windows, Version 4.0
; SEQ ID NO 2037
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-385-692-2037

```

```

Alignment Scores:
Pred. No.: 4.21e-24 Length: 253
Score: 332.00 Matches: 67
Percent Similarity: 51.1% Conservative: 52
Best Local Similarity: 28.8% Mismatches: 108
Query Match: 23.2% Indels: 6
DB: 7 Gaps: 4

```

US-10-608-388a-1 (1-759) x US-11-385-692-2037 (1-253)

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QY 10 TGGGCGATCCTCTCCAGACCGTGTGCTTCTTCAACCTCATCTTCTGGGGGCA 69
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
11 CysGlyThrValCysLeuLysTyLeuLeuPheThrTyAsnCysCysPheTrpLeuAla 30
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
70 GCTGGCATTATGCTATGTGGAGCCCTATGCTTCATCACTTATGATGACTATGACCA 129
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
31 GlyLeuAlaValMetAlaValGlyIleTrpThrLeuAlaLeuLysSerAspTyIleSer 50
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
130 TTCTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTGATCATAGCTGTAGGAGCCCTG 189
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
51 LeuLeuAlaSerGlyThrTyLeuAlaThrAlaTyIleLeuValValAlaGlyThrVal 70
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
190 CTTTTCATCATTTGGCTGCTGTGGCCACAAATCCGGGAAAGTCGCTGTGGACTT 249
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
71 ValMetValThrGlyValLeuGlyCysCysAlaThrPheLysGluArgAsnLeuLeu 90
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
250 GCCAGGTTTGTATCATCTCTGCTCTTGTGTTTGTGCACAGAGTTGTTGTAGTGTGTTG 309

```

```

Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
91 ArgLeuTyThrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 110
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
310 GGATATGTTTACAGAGCAAAAGTGGAAAATGAGTTGATCGCAGCATTCAG---AAAGTG 366
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
111 AlatyAlatyTyTyGlnGlnLeuAsnThrGlnLeuLysGluAsnLeuLysAspThrMet 130
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
367 TATAAGACCTCAATAGGAACCAACCTGCTGCTAGCCGGCTATTGATTATGTATGACAG 426
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
131 ThrLysArgTyHisGlnProGlyHisGlnAlaValThrSerAlaValAspGlnLeuGln 150
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
427 AGACAGCTGCATTTGTTGGAAATTCACAACTACTCAGACTGGGAAAATACAGATTGGTTC 486
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
151 GlnGluPheHisCysCysGlySerAsnAsnSerGlnAspTrpArgAspSerGluTrpIle 170
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
487 AAA-----GAACCAAAAACAGAGTCTCCCTCTTACTGCTGCTCAGAGAGACTGCCAGC 540
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
171 ArgSerGlnGluAlaGlyGlyArgValValProAspSerCysLysValValAla 190
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
541 AATTGTAATGGCAGCTGGCCACCTCCGACCTCTAT-----GCTGAGGGGTGTGAG 594
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
191 LeuCys---GlyGlnArgAspHisAlaSerAsnIleTyLysValGluGlyCysIle 209
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
595 GCTCTAGTAGTGAAGAACTACAAGAAATCATGATGATGATCTGGCGCGCATGGCA 654
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
210 ThrLysLeuGluThrPheIleGlnHisLeuArgValIleGlyAlaValGlyIleGly 229
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
655 TTTCAGCTATTACGCTGCTGGCATGCTGTGTCTTGC 693
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
230 IleAlaCysValGlnValPheGlyMetIlePheThrCys 242

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RESULT 13

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US-11-385-692-2040
; Sequence 2040, Application US/11385692
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: KIDNEY DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL0015910RD
; CURRENT APPLICATION NUMBER: US/11/385,692
; CURRENT FILING DATE: 2006-03-22
; NUMBER OF SEQ ID NOS: 6044
; SOFTWARE: FastSeq for Windows, Version 4.0
; SEQ ID NO 2040
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-385-692-2040

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Alignment Scores:
Pred. No.: 4.21e-24 Length: 253
Score: 332.00 Matches: 67
Percent Similarity: 51.1% Conservative: 52
Best Local Similarity: 28.8% Mismatches: 108
Query Match: 23.2% Indels: 6
DB: 7 Gaps: 4

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US-10-608-388a-1 (1-759) x US-11-385-692-2040 (1-253)

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QY 10 TGGGCGATCCTCTCCAGACCGTGTGCTTCTTCAACCTCATCTTCTGGGGGCA 69
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
11 CysGlyThrValCysLeuLysTyLeuLeuPheThrTyAsnCysCysPheTrpLeuAla 30
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
70 GCTGGCATTATGCTATGTGGAGCCCTATGCTTCATCACTTATGATGACTATGACCA 129
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
31 GlyLeuAlaValMetAlaValGlyIleTrpThrLeuAlaLeuLysSerAspTyIleSer 50
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
130 TTCTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTGATCATAGCTGTAGGAGCCCTG 189
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
51 LeuLeuAlaSerGlyThrTyLeuAlaThrAlaTyIleLeuValValAlaGlyThrVal 70
QY      |||      |||      |||      |||      |||      |||      |||      |||      |||
190 CTTTTCATCATTTGGCTGCTGTGGCCACAAATCCGGGAAAGTCGCTGTGGACTT 249
Db      |||      |||      |||      |||      |||      |||      |||      |||      |||
71 ValMetValThrGlyValLeuGlyCysCysAlaThrPheLysGluArgAsnLeuLeu 90

```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 4, 2006, 21:50:24 ; Search time 3.5 Seconds
(without alignments)
1320.309 Million cell updates/sec

Title: US-10-608-388A-1
Perfect score: 1429
Sequence: 1 atggcgccagtcgagcattcac.....tcactggcggaacctatgca 759

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 361616

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_Spool/US10608388/runat_04042006_150709_14367/app_query.fasta_1
-DB=Published Applications AA New -QFMT=fastan -SUFFIX=n2p.rapbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DICALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs02p
-USER=US10608388@cgn_1_1_24 @runat_04042006_150709_14367 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA_New:

1: /SID55/ptodata/2/pubpaa/US08_NEW_PUB.pcp.*
2: /SID55/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*
3: /SID55/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*
4: /SID55/ptodata/2/pubpaa/PCT_NEW_PUB.pcp.*
5: /SID55/ptodata/2/pubpaa/US05_NEW_PUB.pcp.*
6: /SID55/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
7: /SID55/ptodata/2/pubpaa/US11_NEW_PUB.pcp.*
8: /SID55/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result #No. | Score | Query Match | Length | ID | Description |
|-------------|-------|-------------|--------|----|--------------------|
| 1 | 1336 | 93.5 | 253 | 6 | US-10-501-035-248 |
| 2 | 453 | 31.7 | 222 | 7 | US-11-019-711-81 |
| 3 | 283 | 19.8 | 267 | 6 | US-10-627-952-20 |
| 4 | 283 | 19.8 | 327 | 6 | US-10-821-234-1686 |
| 5 | 282 | 19.7 | 267 | 6 | US-10-329-258-25 |
| 6 | 263 | 18.4 | 241 | 6 | US-10-745-586-35 |
| 7 | 263 | 18.4 | 241 | 7 | US-11-019-711-77 |
| 8 | 263 | 18.4 | 241 | 7 | US-11-019-711-78 |
| 9 | 263 | 18.4 | 241 | 7 | US-11-234-786-114 |

| | | | | | | |
|----|-------|------|------|---|----------------------|-------------------|
| 10 | 251 | 17.6 | 237 | 7 | US-11-108-172-1062 | Sequence 1062, Ap |
| 11 | 251 | 17.6 | 243 | 7 | US-11-108-172-1122 | Sequence 1122, Ap |
| 12 | 251 | 17.6 | 446 | 7 | US-11-108-172-1121 | Sequence 1121, Ap |
| 13 | 250.5 | 17.5 | 282 | 7 | US-11-019-711-80 | Sequence 80, Appl |
| 14 | 234.5 | 16.4 | 344 | 7 | US-11-108-172-1085 | Sequence 1085, Ap |
| 15 | 228 | 16.0 | 240 | 7 | US-11-019-711-76 | Sequence 76, Appl |
| 16 | 226.5 | 15.9 | 247 | 7 | US-11-019-711-79 | Sequence 79, Appl |
| 17 | 218.5 | 15.3 | 227 | 7 | US-11-029-188-6 | Sequence 6, Appl |
| 18 | 218.5 | 15.3 | 228 | 6 | US-10-821-234-1266 | Sequence 1266, Ap |
| 19 | 217 | 15.2 | 241 | 7 | US-11-019-711-22 | Sequence 22, Appl |
| 20 | 196 | 13.7 | 270 | 6 | US-10-453-372-462 | Sequence 462, App |
| 21 | 196 | 13.7 | 270 | 6 | US-10-453-372-464 | Sequence 464, App |
| 22 | 184 | 12.9 | 305 | 6 | US-10-063-703-108 | Sequence 108, App |
| 23 | 184 | 12.9 | 305 | 7 | US-11-102-240-108 | Sequence 108, App |
| 24 | 184 | 12.9 | 305 | 7 | US-11-103-195-108 | Sequence 108, App |
| 25 | 165.5 | 11.6 | 126 | 5 | US-09-978-160A-555 | Sequence 555, App |
| 26 | 146.5 | 10.3 | 204 | 7 | US-11-080-391-8 | Sequence 8, Appl |
| 27 | 143.5 | 9.3 | 172 | 6 | US-10-517-696-108 | Sequence 108, App |
| 28 | 128.5 | 9.0 | 80 | 6 | US-10-475-075-860 | Sequence 860, App |
| 29 | 110.5 | 7.7 | 196 | 6 | US-10-644-807-293 | Sequence 293, App |
| 30 | 107.5 | 7.5 | 273 | 7 | US-11-096-568A-22023 | Sequence 22023, A |
| 31 | 107.5 | 7.5 | 273 | 7 | US-11-096-568A-26249 | Sequence 26249, A |
| 32 | 107.5 | 7.5 | 316 | 7 | US-11-096-568A-22022 | Sequence 22022, A |
| 33 | 107.5 | 7.5 | 317 | 7 | US-11-096-568A-26248 | Sequence 26248, A |
| 34 | 98 | 6.9 | 282 | 7 | US-11-096-568A-23450 | Sequence 23450, A |
| 35 | 97 | 6.8 | 220 | 7 | US-11-096-568A-23451 | Sequence 23451, A |
| 36 | 95.5 | 6.7 | 204 | 7 | US-11-096-568A-23452 | Sequence 23452, A |
| 37 | 93.5 | 6.5 | 1113 | 7 | US-11-067-811-4 | Sequence 4, Appl |
| 38 | 92 | 6.4 | 954 | 6 | US-10-453-372-1150 | Sequence 1150, Ap |
| 39 | 92 | 6.4 | 1268 | 6 | US-10-453-372-1144 | Sequence 1144, Ap |
| 40 | 92 | 6.4 | 1268 | 6 | US-10-453-372-1154 | Sequence 1154, Ap |
| 41 | 92 | 6.4 | 1288 | 6 | US-10-453-372-1146 | Sequence 1146, Ap |
| 42 | 92 | 6.4 | 1288 | 6 | US-10-453-372-1152 | Sequence 1152, Ap |
| 43 | 92 | 6.4 | 1408 | 6 | US-10-453-372-1148 | Sequence 1148, Ap |
| 44 | 89 | 6.2 | 565 | 6 | US-10-055-877-228 | Sequence 228, App |
| 45 | 87.5 | 6.1 | 510 | 7 | US-11-096-568A-34036 | Sequence 34036, A |

ALIGNMENTS

RESULT 1
US-10-501-035-248
; Sequence 248, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTII
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KIN
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 248
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-035-248

Alignment Scores:
Pred. No.: 3 24e-120 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 6 Gaps: 0

US-10-608-388A-1 (1-759) x US-10-501-035-248 (1-253)

QY 1 ATGGCGCCAGTCGCGCATCACCTCTCCAGACCGTGCTGCTTTCTTCAACCTCATCTTC 60

| | | | |
|----|-----|---|-----|
| Db | 1 | MetGlyGlnCysGlyIleThrSerSerIysThrValLeuValPheLeuAsnLeuIlePhe | 20 |
| Qy | 61 | TGGGGGGCAGCTGGCATTTTATGCTATGTGGAGGCTATGCTTTCATCACTTTATGATGAC | 120 |
| Db | 21 | TrpGlyAlaAlaGlyIleLeuCysIyrValGlyAlaIyrValPheIleThrIyrAspAsp | 40 |
| Qy | 121 | TATGNCACACTCTTTGAAGATGTGACAGCTCATCCCTGCTGTAGTGATCATCTGTA | 180 |
| Db | 41 | TyrAspHisPhePheGluAspValIyrThrLeuIleProAlaValValIleIleAlaVal | 60 |
| Qy | 181 | GGAGCCCTGCTTTTCATCATTCGGGCTAATTGGCTGCTGTGCCAATCCGGGAAAGTCGC | 240 |
| Db | 61 | GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysAlaThrIleArgGluSerArg | 80 |
| Qy | 241 | TGTGACHTTGCACGTTTGTGCATCATCTGCTCTTGGTCTTTGTGCACAGAAGTTGTTGA | 300 |
| Db | 81 | CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal | 100 |
| Qy | 301 | GTGTTTGGGATATGTTTACAGAGCAAGGTGGAAATGAGTGTGATCGCAGCATTCAG | 360 |
| Db | 101 | ValValLeuGlyIyrValIyrArgAlaIysValGluAsnGluValAspArgSerIleGln | 120 |
| Qy | 361 | AAAGTGTATAAGACCTCAATGGAAACCAACCTGATGCTGTAGCGGGCTATTGATTAT | 420 |
| Db | 121 | LysValIyrLysThrIyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspIyr | 140 |
| Qy | 421 | GTACAGAGACAGCTGCATTGTTGTGGAATTCACACTACTCAGACTGGGAAAATACAGAT | 480 |
| Db | 141 | ValGlnArgGlnLeuHisCysGlyIleHisAsnIyrSerAspTrpGluAsnThrAsp | 160 |
| Qy | 481 | TGGTTCAAGAAACCAAAACCAGAGTGCCCTCTTAGCTGCTGCAGAGAGACTGCCAGC | 540 |
| Db | 161 | TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer | 180 |
| Qy | 541 | AATTGTAATGGCAGCTGSCCCACCTTCCGACCTCTATGCTAGGGGTGTGAGGCTCTA | 600 |
| Db | 181 | AsnCysAsnGlySerLeuAlaHisProSerAspLeuIyrAlaGluGlyCysGluAlaLeu | 200 |
| Qy | 601 | GTAGTCAGAGAGCTACAGAAATCATGATGATGTGATCTGGCGCGCATTCGATTGCA | 660 |
| Db | 201 | ValValLysLysLeuGlnGluIleMetMetHisValIleIleTrpAlaAlaLeuAlaPheAla | 220 |
| Qy | 661 | GCTATTACAGTCTCGGGATGCTGTGTGCTGCATCGTCTTGTGCAGAGAGGAGTAGAGAT | 720 |
| Db | 221 | AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp | 240 |
| Qy | 721 | CCTGCTTACAGACTCCTCATCATCTGGCGGAACTATGCA | 759 |
| Db | 241 | ProAlaIyrGluLeuLeuIleThrGlyIyrThrAla | 253 |

```

; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shency, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/11/019,711
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/10/037,417
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Tetra
; OTHER INFORMATION: Family Consensus Sequence
US-11-019-711-81

```

US-10-608-388A-1 (1-759) x US-11-019-711-81 (1-222)

| | | | |
|----|-----|---|-----|
| Qy | 28 | AAGACCGTGTGTCCTTCTCAACCTCATCTTCTGGGGGGCAGCTGGCATTTATGCTAT | 87 |
| | | : : : : : : : | |
| Db | 1 | LysTyrLeuLeuPheLeuLeuAsnLeuLeuPheTrpLeuCysGlyIleLeuLeuLeuLeu | 20 |
| | | : : : : : : : | |
| Qy | 88 | GTGGGACCTATGCTTCATCACCATTATCATGACTATGACCACTCTCTTTGAAGATGTGAC | 147 |
| | | : : : : : : : | |
| Db | 21 | ValGlyIleTrpLeuLeuValAspLeuSerSerGluLeuLeuGlySerLeuSer | 40 |
| | | : : : : : : : | |
| Qy | 148 | ACGCTCATCCCTGCTGTAGTGATCATAGCTGTAGAGCCCTGCTTTTCATCATTTGGGCTA | 207 |
| | | : : : : : : : | |
| Db | 41 | SerLeuValAlaIaIaTyrValLeuIleAlaValGlyAlaIleLeuPheLeuValGlyPhe | 60 |
| | | : : : : : : : | |
| Qy | 208 | ATTGGCTGCTGTGCCAATCCGGGAAGTCGCTGTGGAGCTTCCACGTTTCTCATCATC | 267 |
| | | : : : : : : : | |
| Db | 61 | LeuGlyCysCysGlyAlaIleArgGluSerArgCysLeuLeuGlyLeuTyrPheValPhe | 80 |
| | | : : : : : : : | |
| Qy | 268 | CTGCTCTTGTTTTTGTCTACAGAAGTTGTTAGTGGTTTTGGGATATGTTTACAGAGCA | 327 |
| | | : : : : : : : | |
| Db | 81 | LeuLeuLeuIlePheIleLeuGluValAlaIaGlyIleLeuAlaPheValPheArgasp | 100 |
| | | : : : : : : : | |

RESULT 2

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US-11-019-7111-81
; Sequence 81, Application US/11019711
; Publication No. US20060009634A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsbrook II, John P
; APPLICANT: Tschernoy, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothberg, Mark

```



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QY 328 AAGTGGAAATGAGTTGATCGCAGCATTTCAGAAAGTGATATAGACCTCAATGGAC 387
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 388 AACCTGATGCTGCTAGCGGGCTATTGATTATGTACAGACAGCTGCTATTGTGGA 447
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 AspProaspGluArgAsn--AlaTrpAspLysLeuGlnPheLysCysGly 139
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 448 ATTCACAACTACTCAGCTGGGAAATACAGATTGGTTCAAGAAACCAAAACAGAGT 507
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 140 ValAsnGlyThrAspTrpPheAspSerGlnTrpPhe-----SerAsnGly 155
QY 508 GTCCCTCTTACGTGCTGACAGAGAGCTGCCAGCAATTGTAATGCGAGCTGGCCACCT 567
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 156 ValProPheSerCysCysAsnProSerValSer---CysAsnSerAlaGlnAspGlu 174
QY 568 TCCGACCTCTATGCTAGGGGTGTGAGGCTCTAGTAGTGAAGAGCTACAGAAATCATG 627
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 175 AspThrIleTyrGlnGlyCysLeuGlnLysLeuLeuGlnTrpLeuGluGluAsnLeu 194
QY 628 ATGCATGTGCTGGCGGCGACTGGCATTTCAGCTATTTCAGCTGGCGGCTGCTGT 687
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 195 LeuIleValGlyGlyValAlaLeuGlyLeuAlaLeuIleGlnLeuLeuGlyMetIleLeu 214
QY 688 GCTTGCATCGGTGTGTC 705
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 215 SerCysLeuCysCys 220
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
US-10-627-952-20
; Sequence 20, Application US/10627952
; Publication No. US20050250102A1
; GENERAL INFORMATION:
; APPLICANT: Dong, Jin-Tang; Barrett,
; J. Carl; Lamb, Patricia W.; Isaacs, John T.
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND
; GENE THERAPY USING REAGENTS DERIVED FROM THE
; HUMAN METASTASIS SUPPRESSOR GENE KAI1
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,952
; FILING DATE: 24-Jul-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,380
; FILING DATE: 27-Feb-2001
; APPLICATION NUMBER: 09/232,507
; FILING DATE: <UNKNOWN>
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4172US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown

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;
; TOPOLOGY: unknown
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-627-952-20
Alignment Scores:
Pred. No.: 2,59e-19 Length: 267
Score: 283.00 Matches: 78
Percent Similarity: 43.8% Conservative: 41
Best Local Similarity: 28.7% Mismatches: 119
Query Match: 19.8% Indels: 34
DB: Gaps: 7
US-10-608-388A-1 (1-759) x US-10-627-952-20 (1-267)
QY 1 ATGGGCCAGTGGCGGATCACCTCTCAAGACCGTGTGCTCTTCTCAACCTCATCTTC 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 MetGlySerAlaCysIleLysValThrLysTyrPheLeuPheLeuPheLeuLeuPhe 20
QY 61 TGGGGGGCAGCTGGCATTATGCTATGTGGGAGCCTATGCTTTCATCATCTTATGATGAC 120
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 21 PheIleLeuGlyAlaValIleLeuGlyPheGlyValTrpIleLeuAla-----Asp 37
QY 121 TATGACCACTTCTTCAAGATGTGTACAG-----CTCATCCCTGCTGTA 165
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 38 LysSerSerPheIleSerValLeuGlnThrSerSerSerSerLeuArgMetGlyAlaTyr 57
QY 166 GTGATCATAGCTGTAGGAGCCCTGCTTTTCATCATTTGGGCTAATTGGCTGTGTCACACA 225
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 58 ValPheIleGlyValGlyAlaValThrMetLeuMetGlyPheLeuGlyCysIleGlyAla 77
QY 226 ATCCGGGAAAGTCCGCTGTGACCTTGCACGTTTGTTCATCATCTGCTCTTGGTTTGTGTC 285
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 78 ValAsnGluValArgCysLeuLeuGlyLeuTyrPheAlaPheLeuLeuLeuLeuLeu 97
QY 286 ACAGAAAGTTGTTGCTAGTGTGTTTGGATATGTTTACAGACAAAGTGGAAATAGAGTT 345
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 98 AlaGlnValThrAlaGlyAlaLeuPheTyrPheAsnMetGlyLysLeuLysGlnGluMet 117
QY 346 GATCGCAGCATTCAGAAAGTGTATAGACCTACAAATGGAAACCAACCTGTGCTGTAGC 405
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 118 GlyGlyIleValThrGluLeuIleArgAspTyrAsnSerSerArgGluAspSerLeuGln 137
QY 406 CGGGCTATTGATTATGTACAGACAGCTGCTGCTTTGTTGGAATTCACAACTACTCAGAC 465
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 138 AspAlaTrpAspTyrValGlnAlaGlnValLysCysGlyTrpValSerPheTyrAsn 157
QY 466 TGGGAAATACAGATTGGTTCAAGAAACCAAAACACAGAGTGTCCCTCTTGTAGCTGC--- 522
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 158 TrpThrAspAsnAlaGluLeuMetAsnArgProGluValThrTyrProCysSerCysGlu 177
QY 523 -----TGCAGAGAGACTGCC 537
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 178 ValLysGlyGluGluAspAsnSerLeuSerValArgLysGlyPheCys---GluAlaPro 196
QY 538 AGCAATTGTAATGGCAGCTGGCCACCTCCGAC-----CTCTATGCTGAGGGGTGT 591
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 197 GlyAsnArgThrGlnSerGlyAsnHisProGluAspTrpProValTyrGlnGluGlyCys 216
QY 592 GAGGCTCTAGTAGTGAAGAGCTACAGAAATCATCATGATCATGTGTCGGCGGCACTG 651
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 217 MetGluLysValGlnAlaTrpLeuGlnGluAsnLeuGlyIleIleLeuGlyValGlyVal 236
QY 652 GCATTGGACGATTATTCAGCTGCTGGGCATGCTGTGTGCTGTGCTGTGTCGACGAGG 711
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 237 GlyValAlaIleIleGluLeuLeuGlyMetValLeuSer---IleCysLeuCysArgHis 255
QY 712 -----AGTAGAGATCCTGCTTAC 729
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 256 ValHisSerGluAspTyrSerLysValProLysTyr 267
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
US-10-821-234-1686
; Sequence 1686, Application US/10821234

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; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preseclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1686
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1686

Alignment Scores:
Pred. No.: 2,63e-19 Length: 327
Score: 283.00 Matches: 78
Percent Similarity: 43.8% Conservative: 41
Best Local Similarity: 28.7% Mismatches: 119
Query Match: 19.8% Indels: 34
DB: 6 Gaps: 7

US-10-608-388A-1 (1-759) x US-10-821-234-1686 (1-327)
QY 1 ATGGGGCAGTGGCGCATACCTCTCCAGACCGTGTCTTCTCAACCTCATCTTC 60
Db 61 MetGlySerAlaCysIleLysValThrLysTyrPheLeuPheLeuPheAsnLeuIlePhe 80
QY 61 TGGGGGGCAGCTGGCGATTTTATGCTATGCTATGGAGCGCTATGCTTTCATCACTTATGATGAC 120
Db 81 PheIleLeuGlyAlaValIleLeuGlyPheGlyValThrPheLeuAla-----Asp 97
QY 121 TATGACCATTCTTCAAGATGTGTACACG-----CTCATCCCTGCTGTA 165
Db 98 LysSerSerPheIleSerValLeuGlnThrSerSerSerSerSerSerLeuArgMetGlyAlaTyr 117
QY 166 GTGATCATAGCTGTAGAGCCCTGCTTTTCATCATCTTGGCTGTGTTGTTTTC 285
Db 138 ValAsnGluValArgCysLeuLeuGlyLeuTyrPheAlaPheLeuLeuLeuLeuLeu 157
QY 286 ACAGAAAGTTGTTAGTGGTTTGGGATATGTTTACAGACCAAGGTGGAATGAGTT 345
Db 158 AlaGlnValThrAlaGlyAlaLeuPheTyrPheAsnMetGlyLysLeuLysGlnGluMet 177
QY 346 GATCGCAGCATTCAGAAAGTGTATAGCTTCAATGGAACCAACCTCATCTGCTAGC 405
Db 178 GlyGlyIleValThrCluLeuIleArgAspTyrAsnSerSerArgGluAspSerLeuGln 197
QY 406 CGGGCTATTGATATACAGACAGCTGTCATTTGTTGGAATTCACAACTACTCAGAC 465
Db 198 AspAlaTrpAspTyrValGlnAlaGlnValLysCysCysGlyTrpValSerPheTyrAsn 217
QY 466 TGGGAAATACAGATTGGTTTCAAGAAACCAACCAACCAAGGTGCTCTTACGTCG 522
Db 218 TrpThrAspAsnAlaGluLeuMetAsnArgProGluValThrTyrProCysSerCysGlu 237
QY 523 -----TGACAGACGACTGCC 537
Db 238 ValLysGlyGluGluAspAsnSerLeuSerValArgLysGlyPheCys---GluAlaPro 256
QY 538 AGCAATTGTAATGGACCTGGCCCACTTCCGAC-----CTCTATCTCAGGGGTGT 591
Db 257 GlyAsnArgThrGlnSerGlyAsnHisProGluAspTrpProValTyrGlnGluGlyCys 276

US-10-608-388A-1 (1-759) x US-10-329-258-25 (1-267)
QY 1 ATGGGCAGTGGCGCATCACCTCTCCAGACCGTGTGCTTCTCAACCTCATCTTC 60
Db 1 MetGlySerAlaCysIleLysValThrLysTyrPheLeuPheLeuPheAsnLeuIlePhe 20
QY 61 TGGGGGGCAGCTGGCGATTTTATGCTATGCTGAGCGCTATGCTTTCATCACTTATGATGAC 120
Db 21 PheIleLeuGlyAlaValIleLeuGlyPheGlyValThrPheLeuAla-----Asp 37
QY 121 TATGACCATTCTTGTGAAGATGTGTACACG-----CTCATCCCTGCTGTA 165
Db 38 LysSerSerPheIleSerValLeuGlnThrSerSerSerSerSerSerLeuArgMetGlyAlaTyr 57
QY 166 GTGATCATAGCTGTAGAGCCCTGCTTTTCATCATCTTGGCTGTGTTGTTTTC 225
Db 58 ValPheIleGlyValGlyAlaValThrMetLeuMetGlyPheLeuGlyCysIleGlyAla 77
QY 226 ATCCGGGAAGTCGCTGGGACTTGGCCACGTTTGTGCATCATCTCTCTGTTGTTTTC 285
Db 78 ValAsnGluValArgCysLeuLeuGlyLeuTyrPheAlaPheLeuLeuLeuLeuLeu 97
QY 286 ACAGAAAGTTGTTAGTGGTTTGGGATATGTTTACAGACCAAGGTGGAATGAGTT 345
Db 98 AlaGlnValThrAlaGlyAlaLeuPheTyrPheAsnMetGlyLysLeuLysGlnGluMet 117
QY 346 GATCGCAGCATTCAGAAAGTGTATAGACCTTACATGGAACCAACCTCATCTGCTAGC 405
Db 118 GlyGlyIleValThrGluLeuIleArgAspTyrAsnSerSerArgGluAspSerLeuGln 137
```


APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/11/019,711
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US/10/037,417
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 77
LENGTH: 241
TYPE: PRT
ORGANISM: Homo sapiens
US-11-019-711-77

Alignment Scores:
Pred. No.: 241
Score: 263.00 Matches: 68
Percent Similarity: 46.5% Conservative: 45
Best Local Similarity: 28.0% Mismatches: 114
Query Match: 18.4% Indels: 16
DB: 7 Gaps: 6

US-10-608-388A-1 (1-759) x US-11-019-711-77 (1-241)

7 CAGTGGCGGATCACCTCTCCAGACCGTGGTCTTCTCAACCTCATCTCTGGGGG 66
2 GlnCys---PheSerPheIleLysThrMetMetIleLeuPheAsnLeuIlePheLeu 20
67 GCAGTGGCAATTTATGTATGGGAGCCTATGCTTCATCATCTATGAGACTATGAC 126
21 CysGlyAlaAlaLeuAlaValGlyIleTrpValSerIleAspGlyAlaSerPheLeu 40
127 CACTCTTTGAAGATGTACACGCTCATCCCTGCTGTAGTG-----ATC 171
41 LysIlePheGlyProLeuSerSerAlaMetGlnPheValAsnValGlyTyrPheLeu 60
172 ATAGCTGAGGAGCCTGCTTTTCATCATTTGGCTAAATGGTGTGCTGCCAATCCGG 231
61 IleAlaAlaGlyValValPheAlaLeuGlyPheLeuGlyCysTyrGlyAlaLysThr 80
232 GAAAGTCGCTGGAGCTGCCAGTTTGTATCATCTGCTCTTGGTTTGTCTACAGAA 291
81 GluSerLysCysAlaLeuValThrPhePheIleLeuLeuIlePheIleAlaGlu 100
292 GTTGTGTAGTGTGGATATTTTACAGACCAAGGTGGAATGAGGCTTCATCGC 351
101 ValAlaAlaValAlaLeuValTyrThrMetAlaGluHisPheLeuThrLeu 120
352 AGCATTGAGAAAGTGTATAGACCTACAATGGAACCAACCTGATGCTAGCCGGCT 411

121 LeuValValProAlaIleLysLysAspTyrGlySerGlnGluAsp---PheThrGlnVal 139
412 ATTGATTATGTACAGACAGACTGCTGATTGTTGTGGATTACACTACTACTACAGTGGAA 471
140 TrpAsnThrThrMetLysGlyLeuLysCysGlyPheThrAsnTyrThrAspPheGlu 159
472 AATACAGATTGGTTCAAGAAACCAAAACACAGAGTGTCCCTCTTAGCTGTGCAGAGAG 531
160 AspSerProTyrPheLysGlu-----AsnSerAlaPheProPheCysAsnAsp 177
532 ACTCCAGCAAT-----TGTAAATGGACGCTGGCCACCTTCCAGCTC 576
178 AsnValThrAsnThrAlaAsnGluThrCysThrGluGlnLysAlaHis-----AspGln 195
577 TATCTGAGGGGTGTGAGGCTCTAGTAGTGAAGAGCTACAAGAAATCATGATGATGCTG 636
196 LysValGluGlyCysPheAsnGlnLeuLeuTyrAspIleArgThrAsnAlaValThrVal 215
637 ATCTGGGCGGCACTGGCAATTTGCAGCTATTTCAGCTGTGGGCATGCTGTGCTTGCATC 696
216 GlyGlyValAlaAlaGlyIleGlyLeuGluLeuAlaAlaMetIleValSerMetTyr 235
697 GTGTTGTGC 705
236 LeuTyrCys.238

RESULT 8

US-11-019-711-78
Sequence 78, Application US/11019711
Publication No. US20060009634A1

GENERAL INFORMATION:

APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Patturajan, Meera
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Vernet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Perenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/11/019,711
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US/10/037,417
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186

| | | | | | |
|---|---------------------------|---|-----|--|--|
| | | | | | |
| : | PRIOR FILING DATE: | 2001-05-15 | | | |
| : | PRIOR APPLICATION NUMBER: | 60/303,231 | | | |
| : | PRIOR FILING DATE: | 2001-07-05 | | | |
| : | PRIOR APPLICATION NUMBER: | 60/305,060 | | | |
| : | PRIOR FILING DATE: | 2001-07-12 | | | |
| : | PRIOR APPLICATION NUMBER: | 60/318,405 | | | |
| : | PRIOR FILING DATE: | 2001-09-10 | | | |
| : | PRIOR APPLICATION NUMBER: | 60/318,700 | | | |
| : | PRIOR FILING DATE: | 2001-09-12 | | | |
| : | NUMBER OF SEQ ID NOS: | 227 | | | |
| : | SOFTWARE: | PatentIn Ver. 2.1 | | | |
| : | SEQ ID NO 78 | | | | |
| : | LENGTH: | 241 | | | |
| : | TYPE: | PRT | | | |
| : | ORGANISM: | Homo sapiens | | | |
| : | US-11-019-711-78 | | | | |
| | | | | | |
| Alignment Scores: | | | | | |
| Pred. No.: | 2,12e-17 | Length: | 241 | | |
| Score: | 263.00 | Matches: | 68 | | |
| Percent Similarity: | 46.5% | Conservative: | 45 | | |
| Best Local Similarity: | 28.0% | Mismatches: | 114 | | |
| Query Match: | 18.4% | Indels: | 16 | | |
| DB: | 7 | Gaps: | 6 | | |
| | | | | | |
| US-10-608-388A-1 (1-759) x US-11-019-711-78 (1-241) | | | | | |
| QY | 7 | CAGTGGCGGCATACCCCTCCCAAGACCGTGCTGTTCTTCTCAAACCTCATCTTCCTGGGG | 66 | | |
| Db | 2 | GlnCys---PheSerPheIleLysThrMetMetIleLeuPheAsnLeuLeuIlePheLeu | 20 | | |
| QY | 67 | GCAGCTGGCATTTTATGTCTATGTGGAGCGCTATGTCTTCATCACCTATTATGACTATGAC | 126 | | |
| Db | 21 | CysGLyAlaAlaLeuAlaValGLyIletrpValSerIleAspGLyAlaSerPheLeu | 40 | | |
| QY | 127 | CACCTCTTTGAAGATGTGTACAGCTCATCCCTGCTGTAGTG-----ATC | 171 | | |
| Db | 41 | LysIlePheGLyProLeuSerSerSerAlaMetGlnPheValAsnValGLyTyrPheLeu | 60 | | |
| QY | 172 | ATAGCTGTAGGACCGCTGTTTTTCATCTTTTGGCTTAATGGCTGCTGTGCCACAATCCGG | 231 | | |
| Db | 61 | IleAlaALaGLyValvalvalPhealaleuglyPheleuglyCysTyrGLyAlaLysThr | 80- | | |
| QY | 232 | GAAGTCGCTGTGGACTGCCACGTTTGTCATCATCTGCTGTTGGTTTTGTGCACAGA | 291 | | |
| Db | 81 | GIuSerLYsCysAlaLeuValThrPhePhePheIleLeuLeuLeuIlePheIleAlaGLu | 100 | | |
| QY | 292 | GTITGTTAGTGGTTTGGGATATGTTTACAGACCAAGTGGAAATAGGTTGATCGC | 351 | | |
| Db | 101 | ValAlaAlaAlaValAlaLeuValTyrThrMetAlaGLuHisPheLeuThrLeu | 120 | | |
| QY | 352 | AGCATTCAGAAAAGTGTATAGACCTACAATGGAACCAACCTGATGCTGTAGCCGGCT | 411 | | |
| Db | 121 | LeuValValProAlaIleLysLysaspTyrGLyserGlnGluAsp----PheThrGlnVal | 139 | | |
| QY | 412 | ATTGATTATGTACAGACAGCTGCATGTTGTTGGATTTCACAACTACTACTAGACTGGGAA | 471 | | |
| Db | 140 | TrpAsnThrThrMetLysGLyLeuLysCysCysGLyPheThrAsnTyrThrAspPheGlu | 159 | | |
| QY | 472 | AATACAGATTGGTTCAAGAAACCANAACACAGAGTGCCTCTTAGCTCTCGACAGAG | 531 | | |
| Db | 160 | AspSerProTyR-PheLysGlu-----AsnSerAlaPheProPheCysCysAsnAsp | 177 | | |
| QY | 532 | ACTGCCAGCAAT-----TGTAATGGCAGCCTGGCCCCACCCCTCCGACCTC | 576 | | |
| Db | 178 | AsnValThrAsnThrAlaAsnGluThrCysThrLysGlnLysAlaHis-----AspGln | 195 | | |
| QY | 577 | TATGCTGAGGGGTGTGAGGCTCTACTGTGAGAAGCTTACAAGAAATCATGATGCATGTG | 636 | | |
| Db | 196 | LysValGLUGLyCysePheAsnGlnLeuLeuTyrAspIleargThrAsnAlaValThrVal | 215 | | |
| QY | 637 | ATCTGGCGCCACTGGCATTTTGCAGCTATTTCAGCTGTGGCGCATGTGTTGCTGCATC | 696 | | |

Db 2 GlnCys---PheSerPheIleLysThrMetMetIleLeuPheAsnLeuLeuIlePheLeu 20
QY 67 GCAGCTGGCAATTTATGCTATGGGAGCCTATGCTTCTCATCTATGATCATCATGAC 126
Db 21 CysGlyAlaAlaLeuLeuAlaValGlyIleTrpValSerIleAspGlyAlaSerPheLeu 40
QY 127 CACTTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTG-----ATC 171
Db 41 LysIlePheGlyProLeuSerSerSerAlaMetGlnPheValAsnValGlyTyrPheLeu 60
QY 172 ATAGCTGTAGGACCCCTGCTTTTCATCATTTGGCTAAATGGCTGTGTGCCACAATCCGG 231
Db 61 IleAlaAlaGlyValValPheAlaLeuGlyPheLeuGlyCysTyrGlyAlaLysThr 80
QY 232 GAAAGTCGCTGGACTGCCAGCTTGTTCATCATCTGCTCTGCTGTTTGTTCACAGAA 291
Db 81 GluSerLysCysAlaLeuValThrPhePheIleLeuLeuLeuIlePheIleAlaGlu 100
QY 292 GTTGTGTAGTGTGTTGGGATATGTTTACAGACGAAAGGTGAAATGAGGTTCATCGC 351
Db 101 ValAlaAlaAlaValValAlaLeuValThrThrMetAlaGluHisPheLeuThrLeu 120
QY 352 ASCATTTCAGAAAGTGTATAGACCTACATGAACCAACCCCTGCTGTAGCCGGCT 411
Db 121 LeuValValProAlaIleLysLysAspTyrGlySerGlnLysAsp---PheThrGlnVal 139
QY 412 ATGTATTATGACAGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 471
Db 140 TrpAsnThrThrMetLysGlyLeuLysCysGlyPheThrAsnTyrThrAspPheGlu 159
QY 472 AATCAGATGTGTTCAAAAGAAACCAAAACCAAGAGTGTCCCTCTTAGCTGTGCGCAGAG 531
Db 160 AspSerProTyrPheLysGlu-----AsnSerAlaPheProPheCysCysAsnAsp 177
QY 532 ACTGCCAGCAAT-----TCTAATGGCAGCCTGGCCACCTTCCGACCTC 576
Db 178 AsnValThrAsnThrAlaAsnGluThrCysThrLysGlnLysAlaHis-----AspGln 195
QY 577 TATGCTGAGGGGTGCTGAGGCTGTAGTAGTGAAGAGCTACAGAAATCATGATGATG 636
Db 196 LysValGluGlyCysPheAsnGlnLeuLeuTyrAspIleArgThrAsnAlaValThrVal 215
QY 637 ATCTGGCGCGCATGCAATTTGAGCTATTCAGCTGCTGGGATGCTGTGTGCTTGCATC 696
Db 216 GlyGlyValAlaAlaGlyIleGlyGlyLeuGluLeuAlaAlaMetIleValSerMetTyr 235
QY 697 GTGTTGTGC 705
Db 236 LeuTyrCys 238

RESULT 10

US-11-108-172-1062
; Sequence 1062, Application US/11108172
; Publication No. US20050260177A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Fuduo
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.471C15
; CURRENT APPLICATION NUMBER: US/11/108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1062
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-108-172-1062

Alignment Scores:

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|------------------------|----------|---------------|-----|
| Pred. No.: | 2,99e-16 | Length: | 237 |
| Score: | 251.00 | Matches: | 66 |
| Percent Similarity: | 49.6% | Conservative: | 48 |
| Best Local Similarity: | 28.7% | Mismatches: | 94 |
| Query Match: | 17.6% | Indels: | 22 |
| DB: | 7 | Gaps: | 8 |

US-10-608-388A-1 (1-759) x US-11-108-172-1062 (1-237)

| | | | |
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| QY | 49 | AACCTCATCTTCTGGGGGAGCTGGCAATTTATGCTATGTTGGGAGCCTATGCTTCTATC | 108 |
| Db | 16 | AsnPheLeuPheTrpLeuCysGlyIleLeuAlaLeuAlaIleTrpValArgVal | 35 |
| QY | 109 | ACTTATGATGACTATGACCACTTC---TTTGAAGATGTG-----TACAGCTCATCCCT | 159 |
| Db | 36 | SerAsnAspSerGlnAlaIlePheGlySerGluAspValGlySerSerTyrValAla | 55 |
| QY | 160 | GCTGTAGTATGATGATGCTAGGAGCCCTGCTTTTTCATCTATGTTGGGCTAATTCGCTGT | 219 |
| Db | 56 | ValAspIleLeuIleAlaValGlyAlaIleIleMetIleLeuGlyPheLeuGlyCysCys | 75 |
| QY | 220 | GCCACAATCCGGGAAGTCGCTGTGAGCTGCCAGCTTGTGCATCATCTGCTCTTGTGT | 279 |
| Db | 76 | GlyAlaIleLysGluSerArgCysMetLeuLeuPhePheIleGlyLeuLeuLeuIle | 95 |
| QY | 280 | TTTGTACAGAAAGTTGTTGTAGTGTGTTTGGATATGTTTACAGACCAAGGTGGAAAT | 339 |
| Db | 96 | LeuLeuLeuGlnValAlaThrGlyIleLeuGlyAlaValPheLysSerLysSerArg | 115 |
| QY | 340 | GAGGTTGATCGCAGCATTCAGAAAGTGTATAGACCTACAATGGAACCAACCTGATGCT | 399 |
| Db | 116 | IleValAsnGluThrLeuTyrGluAsnThrLysLeuLeuSerAlaThrGlyGluSerGlu | 135 |
| QY | 400 | GCT-----AGCCGGGCTATTGATTATGTACAGACAGACTGCTCATTTGTGTGAATTCAC | 453 |
| Db | 136 | LysGlnPheGlnGluAlaIleIleValPheGlnGluPheLysCysGlyLeuVal | 155 |
| QY | 454 | AAC---TACTCAGACTGGGAAATATACAGATTGGTTTCAAGAAACCAACCAAGAGTGT | 510 |
| Db | 156 | AsnGlyAlaAlaAspTrpGlyAsn-----AsnPheGlnHisTyr | 168 |

APPLICANT: Clapper, Jonathan D.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedwick Thomas S.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C15
CURRENT APPLICATION NUMBER: US/11/108,172
CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 10/025,380
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 09/922,217
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 09/833,263
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 09/649,811
PRIOR FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: US 09/609,448
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/575,251
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/519,444
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: US 09/504,629
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: US 09/480,321
PRIOR FILING DATE: 2000-01-10
PRIOR APPLICATION NUMBER: US 09/476,296
PRIOR FILING DATE: 1999-12-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1130
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1121
LENGTH: 446
TYPE: PRT
ORGANISM: Homo sapiens
US-11-108-172-1121

Alignment Scores:
Pred. No.: 3,15e-16 Length: 446
Score: 251.00 Matches: 66
Percent Similarity: 49.6% Conservative: 48
Best Local Similarity: 28.7% Mismatches: 94
Query Match: 17.6% Indels: 22
DB: 7 Gaps: 8

US-10-608-388A-1 (1-759) x US-11-108-172-1121 (1-446)

QY 49 AACCTCATCTTCTGGGGGCGAGCTGCAATTTATGCTATGTGGAGCCCTATGCTTCATC 108
DB 219 AsnPheLeuPheTrpLeuCysGlyIleLeuLeuLeuAlaIleTrpValArgVal 238
QY 109 ACTTATGATGACTATGACCACTTC---TTTGAAGATGTG-----TACAGCTCATCCCT 159
DB 239 SerAsnAspSerGlnAlaIlePheGlySerGluAspValGlySerSerTrpValAla 258
QY 160 GCTGTAGTATGATCATGCTAGAGCCCTGCTTTTCATCATTTGGGCTAATGCTGCTGT 219
DB 259 ValAspIleLeuIleAlaValGlyAlaIleIleMetIleLeuGlyPheLeuGlyCysCys 278
QY 220 GCCAATCGGGAAGTGTCTGTGACCTGACCTGACCTTGTCTATCATCTGCTCTTGGTT 279
DB 279 GlyAlaIleLysGlySerArgCysMetLeuLeuLeuPhePheIleGlyLeuLeuIle 298
QY 280 TTGTGCACAGAAGTGTGTAGTGGTGTGGGATATGTTTACAGACAAAGGTGGAAT 339
DB 299 LeuLeuLeuGlnValAlaThrGlyIleLeuGlyAlaValPheLysSerLysSerAspArg 318
QY 340 GAGTTGATCGGACATTCAGAAAGTGTATAGACCTTACAACTGGAACCAACCTGTATGCT 399
DB 319 IleValAsnGluThrLeuTrpGluAsnThrLysLeuLeuSerAlaThrGlyGluSerGlu 338

QY 400 GCT-----AGCCGGCTATTGATTATGTACAGACAGAGCTGCAATTTGTTGGAATTCAC 453
DB 339 LysGlnPheGlnGluAlaIleIleValPheGlnGluGluPheLysCysCysGlyLeuVal 358
QY 454 AAC---TACTCAGACTGGGAAATAACAGATTGGTTTCAAAGAAACCAAAACACAGAGTGTTC 510
DB 359 AsnGlyAlaAlaAspTrpGlyAsn-----AsnPheGlnHisTyr 371
QY 511 CCTCTTAGCTGC---TGCAGAGAGACTGCCAGCAATTCG-----AATGGCAGCCTG 558
DB 372 ProGluLeuCysAlaCysLeuAspLysGlnArgProCysGlnSerTyrAsnGly----- 389
QY 559 GCCACACCTTCGACCTCTATGCTGAGGGGTGTGAGGCTCTAGTAGTAGTGAAGAAGCTACAA 618
DB 390 -----LysGlnValTyrLysGluThrCysIleSerPheIleLysAspPheLeuAla 406
QY 619 GAATCATGATGATGATGATCTGGGCCGACACTGGGCAATTTGAGCTATTTCAGCTGCTGGGC 678
DB 407 LysAsnLeuIleIleValIleGlyIleSerPheGlyLeuAlaValIleGluIleLeuGly 426
QY 679 ATGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 708
DB 427 LeuValPheSerMetValLeuTrpCysGln 436
RESULT 13
US-11-019-711-80
Sequence 80, Application US/11019711
Publication No. US20060009634A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Patturajan, Meera
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Vernet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigar, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/11/019,711
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US/10/037,417
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05

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; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-11-019-711-80

Alignment Scores:
Pred. No.: 3,39e-16 Length: 282
Score: 250.50 Matches: 67
Percent Similarity: 41.5% Conservative: 50
Best Local Similarity: 23.8% Mismatches: 108
Query Match: 17.5% Indels: 57
DB: 7 Gaps: 11

US-10-608-388A-1 (1-759) x US-11-019-711-80 (1-282)
Qy 1 ATGGGCCAGTGGCGCATCACCTCTCCAGAGCCGTGGTCTTTCTCAACCTCATCTTC 60
Db 1 MetGlySerCys---ValAsnAlaLeuArgileValThrPheLeuPheAsnPhaAlaPhe 19
Qy 61 TGGGGGGCAGCTGGCATTTATGCTATGTGGAGCCGTATGCTTCATCAGCTATATGAGAC 120
Db 20 Trp---LeuSerGlyValValPhe---GlyLeuGlyileTrpLeuLeuPheAsnPro 37
Qy 121 TATGACCACTTCTTGAAGATGTGTACAGCTCATCCCTGCTGTA----- 165
Db 38 AlaAlaSerAppPheAlaLeuHisSerThrHisProGlyAlaPheArgTyrValGly 57
Qy 166 ---GTGATCAPAGCTAGGAGCCCTGCTTTTCATCATTTGGCTTAATTTGGCTGTGCC 222
Db 58 TrpPheLeuValGlyAlaGlyAlaileileileLeuValGlyTyrPheGlyCysileGly 77
Qy 223 ACAATCCGGGAAAGTCGTGGAGCTGCCAGTTTGTTCATCATCTGCTCTTGGTTTTT 282
Db 78 AlaTrpLysMetAsnGlnCysAlaLeuAlaPhePheCysCysileLeuLeuAlaPhe 97
Qy 283 GTCACAGAAGTTGTTGGATGTTTGGATGTTTACAGAGCAAGAGTGGAAAGAGAG 342
Db 98 PheLeuGluLeuAlaAlaAlaValThrLeuPheHisLysGlnGluHisileLysHisTyr 117
Qy 343 GTTGATCGCAGCATTCAGAAAGTGTATAAGACCTACAATGGA-----ACCAACCTCAT 396
Db 118 ValGluSerSer-----MetTyrAspThrileArgAsnArgTyrSerSerGluThr 134
Qy 397 GCTGCTAGCCGGCTATTGATATGTACAGAGAGCTGCATTTGTTGGAAATTCACAAC 456
Db 135 AlaPheLysAspAlaPheAspThrValGlnLulysPheGluCysCysGlyValLysThr 154
Qy 457 TACTCAGACTGGAAATACAGATGTTTCAAGAAACCAACCAACACCG----- 504
Db 155 TyrThrAspTrpLeuSerAlaArgTrpAspAlaGluProSerThrGlnLeuGluValAsn 174
Qy 504 ----- 504
Db 175 GluGluAspAlaGlyArgileGluHisGlyileGlyAlaPheGlyGlyAsnLysGlyThr 194
Qy 505 -----AGTGTCCCTTGTAGTGTGTGCAGAGAGACTGCC-----AGC 540
Db 195 GlyTyrGlyArgValProSerSerCysCysAsnGluHisGlyLysLeuSerTyrProAsn 214
Qy 541 AATTGTAATGGACCTGGCCAC---CCITCCACCTCTCTGCTGAG----- 585
Db 215 AsnCysGlyArgSerPheSerGlnAlaProLeuAsnThrTyrAlaGlnPheileAsnThr 234
Qy 586 ---GGGTGTGAGGCTCTAGTAGTGAAGAGCTACAAGAAATCATGATGATGATCTGG 642
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Db 235 ArgGlyCysAlaAspAlaValTyrGluSerValSerSerLeuSerLeuValGly 254
Qy 643 GCCGACTGGCATTTGCAGCTATTATTCAGCTCTGGGCGATG-----CTGTGT 687
Db 255 ValCysValValLeuCysileValGlnLeuLeuGlyileValLeuSerMetThrLeuCys 274
Qy 688 GCTTGC 693
Db 275 CysCys 276

RESULT 14
US-11-108-172-1085
; Sequence 1085, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C15
; CURRENT APPLICATION NUMBER: US/11/108,172
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1085
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-108-172-1085

Alignment Scores:
Pred. No.: 1.17e-14 Length: 344
Score: 234.50 Matches: 60
Percent Similarity: 50.5% Conservative: 41
Best Local Similarity: 30.0% Mismatches: 78
Query Match: 16.4% Indels: 21
DB: 7 Gaps: 7
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US-10-608-388A-1 (1-759) x US-11-108-172-1085 (1-344)

QY 136 GAAGATGTG-----TACAGCTCATCTCTGTGTAGTATGATCATGCTAGAGCCCTG 189
Db 153 GluapValGlySerSerSeryrValAlaValaspIleLeuAlaValGlyAlaIle 172
QY 190 CTTTTCATATGGCTTAATGGCTCTGTGCCAATCCGGGAAGTCGCTGTGACTT 249
Db 173 IleMetIleuGlyPheLeuGlyCysGlyAlaIleGlySerArgCysMetLeu 192
QY 250 GCCACCTTTGTTCATCTCTCTCTGTGTTTGTTCACAGAAGTCTGTGTGTTG 309
Db 193 LeuLeuPhePheIleGlyLeuLeuLeuIleLeuLeuGlnValAlaThrGlyIleLeu 212
QY 310 GGATATGTTTACAGACAAAGTGGAAATAGGTGTGTCGAGCATTCAGAAAGTGTAT 369
Db 213 GlyAlaValPheLeuGlySerSeryrValAlaValaspIleLeuLeuGlnValAlaThrGlyIleLeu 232
QY 370 AGACCTACATGACCAACCACTGATGCTGCT-----AGCCGGCTATTGATTATGTA 423
Db 233 LysLeuLeuSerAlaThrGlyGluSerGluLysGlnPheGlnGluAlaIleValPhe 252
QY 424 CAGACAGCTGCTATTGTTGTGAATTCACAAC---TACTCAGACTGGGAAATACAGAT 480
Db 253 GlnGluGluPheLeuGlyCysGlyLeuValAsnGlyAlaAlaAspTrpGlyAsn----- 270
QY 481 TGGTTCAAGAAACCAAAACAGAGTGCCTCTTGTAGTGC---TGCAGAGAGACTGCC 537
Db 271 -----AsnPheGlnHisTyrProGluLeuCysAlaCysLeuAspLysGln 285
QY 538 AGCAATTGT-----AATGCAGCCTGGCCACCCTCTCCGACCTCATGCTGAGGG 588
Db 286 ArgProCysGlnSerTyrAsnGly-----LysGlnValTyrLysGluThr 300
QY 589 TGTGAGGCTCTAGTGAAGAAGCTACAGAAATCATGATCATGCTGTGCTGGGCGCA 648
Db 301 CysIleSerPheIleLysPheLeuAlaLysAsnLeuIleIleValIleGlyIleSer 320
QY 649 CTGGCATTTCAGCTATTACGCTGTGGGAGCTGTGTGCTGCTGCTGCTGCTGCTG 708
Db 321 PheGlyLeuAlaValIleGluIleLeuGlyLeuValPheSerMetValLeuTyrCysGln 340

RESULT 15
US-11-019-711-76
; Sequence 76, Application US/11019711
; Publication No. US2006009634A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Rameesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldo, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E

; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/11/019,711
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/10/037,417
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-019-711-76

Alignment Scores:
Pred. No.: 4,79e-14 Length: 240
Score: 228.00 Matches: 64
Percent Similarity: 46.0% Conservative: 46
Best Local Similarity: 26.8% Mismatches: 107
Query Match: 16.0% Indels: 22
Ds: 7 Gaps: 7

US-10-608-388A-1 (1-759) x US-11-019-711-76 (1-240)

QY 28 AAGACCGTGTGCTTCTTCAACCTCATCTCTCGGGCGGCGCTGGCATTTATGCTAT 87
Db 8 LysValMetMetPheLeuPheAsnLeuLeuPheLeuCysGlyAlaAlaLeuLeuAla 27
QY 88 GTGGAGCCTATGCTTTCATCATGATGATGATGATGATGATGATGATGATGATGAT 147
Db 28 ValGlyIleTrpValSerValAspGlyThrSerPheLeuLysValPheGlySerLeuSer 47
QY 148 AGCTCATCTCTGCTGTAGTG-----ATCATAGCTGTAGGAGCCCTGCTT 192
Db 48 SerSerAlaMetGlnPheValAsnValGlyTyrPheLeuIleAlaAlaGlyAlaValLeu 67
QY 193 TTCATCTGGCTAATTTGGCTGTGTCACCAATCCGGGAAGTCGCTGTGAGCTTGC 252
Db 68 PheIleLeuGlyPheLeuGlyCysTyrGlyAlaHisSerGluAsnLysCysValLeuMet 87
QY 253 AGTTTGTTCATCTCTCTCTGTTTGTTCACAGAAGTGTGTGTGTGTGTGTGTGTGGA 312
Db 88 MetPhePheSerIleLeuLeuIlePheIleAlaGluIleAlaGlyAlaValValAla 107
QY 313 TATGTTTACAGACCAAGTGTGGAAT-----GAGTTTCATCGCAGCTTCAG 360
Db 108 LeuValTyrThrLeuAlaGluGlnPheLeuThrLeuLeuValValProAlaIleGlu 127
QY 361 AAAGTGTATAAGACCTACATGGAACCAACCTGATGCTGTAGCGGGCTATTGATTAT 420
Db 128 LysAspTyr-----GlyTyrGlnThrAsp---PheThrGlnValTrpAsnThr 142
QY 421 GTACAGACAGCTGCTATTGTTGTGGAATTCACACTACTACAGCTGGGAAATACAGAT 480
Db 421 GTACAGACAGCTGCTATTGTTGTGGAATTCACACTACTACAGCTGGGAAATACAGAT 480

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Db 143 ThrMetGluGluLeuHisCysCysGlyPheAsnAsnTyrThrAspPheAsnAlaSerArg 162
Qy 481 TGGTTCAAGAAACCAAAACCCAGAGTGTCCCTCTTAGCTGCTGC-----AGA 528
Db 163 PheValLysGlu-----AsnLysValPheProProCysCysAlaAsnProGlyAsn 180
Qy 529 GAGACTGCCAGCAATTGTAATGGCAGCCTGGGCCACCCCTTCGACCTCTATGCTGAGGGG 588
Db 181 HisThrValGluProCysThrGluGluLysAla-----LysSerMetLysValGlnGly 198
Qy 589 TGTGAGGCTCTAGTAGTGAAGAGCTACAAGAAATCATGATGCATGCTGAGCCGCCA 648
Db 199 CysPheLysGluIleLeuHisArgIleArgAlaAsnAlaValThrValGlyGlyValAla 218
Qy 649 CTGGCAATTTCAGCTATTTCAGCTGCTGGGCATGCTGTGTGCTTGCATCGTGTGTGTC 705
Db 219 ValGlyValAlaAlaLeuGluLeuAlaAlaMetValValSerMetTyrLeuTyrCys 237
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Search completed: April 4, 2006, 21:56:04
Job time : 23.5 secs

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☐ GRAY SCALE DOCUMENTS

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☐ OTHER: _____

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